



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105257

TO: Phillip Gambel
Location: CM-119E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/155739

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gambel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:01:50 ; Search time 53.6727 Seconds
(without alignments)
363.748 Million cell updates/sec

Title: US-09-155-739-11

Perfect score: 655

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYMDYWGQGITLVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	123	16	Humanized VLA-4 an
2	655	100.0	142	16	Human VLA-4 reshap
3	655	100.0	142	18	Humanised alpha-4
4	648	98.9	123	18	Humanised alpha-4
5	552	84.3	123	16	Mouse anti-VLA-4 a
6	544	83.1	140	16	Mouse VLA-4 antibo
7	544	83.1	140	18	Mouse anti-VLA-4 a
8	523.5	79.9	120	19	Alpha-4 integrin m
9	523.5	79.9	120	23	Heavy chain variab
					Humanised antibody

10	523.5	79.9	431	22	AAS30693	A fusion of single
11	523	79.8	136	16	AAW76681	Human/murine chime
12	523	79.8	136	17	AAW04396	Chimaeric human/mu
13	523	79.8	269	16	AAW76682	Human ONS-M21 anti
14	523	79.8	269	17	AAW04397	Chimaeric human/mu
15	515	78.6	119	16	AAW81325	Humanized VLA-4 an
16	515	78.6	119	18	AAW22426	Humanized alpha-4
17	512	78.2	119	16	AAW81324	Humanized VLA-4 an
18	512	78.2	119	18	AAW22425	Humanized alpha-4
19	507.5	77.5	135	21	AAW07969	A heavy chain vari
20	505.5	77.2	258	23	ABW05963	Monoclonal antibody
21	505.5	77.2	258	23	ABW05992	Mouse and human ch
22	505.5	77.2	258	23	ABW05996	Human monoclonal a
23	504.5	77.0	118	14	AAW37611	Human monoclonal a
24	503	76.8	119	20	AAW52717	hIL2R Ab H chain V
25	503	76.8	119	22	AAW74978	Humanised ATR-5 H
26	501.5	76.6	258	23	ABW05991	Humanised ATR-5 H
27	501.5	76.6	258	23	ABW05995	Mouse and human ch
28	499	76.2	119	20	AAW52719	Human monoclonal a
29	499	76.2	119	22	AAW74980	Humanised ATR-5 H
30	496	75.7	136	17	AAW92084	Humanised antibody
31	496	75.7	136	23	ABG31443	Amino acid sequenc
32	495	75.6	119	16	AAW81331	Human 2*CL antibod
33	493	75.3	119	20	AAW52718	Humanised ATR-5 H
34	493	75.3	119	22	AAW74979	Humanised ATR-5 H
35	492	75.1	117	15	AAW57476	CDR-grafted anti-R
36	492	75.1	117	17	AAW92079	Murine 1308F VH CD
37	492	75.1	117	23	ABG31426	Humanised CDR-graf
38	492	75.1	136	15	AAW37481	Humanised 1308F VH
39	491.5	75.0	245	23	ABP45885	Human Blys binding
40	491	75.0	119	20	AAW52708	Humanised ATR-5 H
41	491	75.0	119	22	AAW74969	Humanised ATR-5 H
42	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
43	489	74.7	119	20	AAW52720	Humanised ATR-5 H
44	489	74.7	119	22	AAW74981	Humanised ATR-5 H
45	487.5	74.4	120	15	AAW47491	Humanised anti-CD1

ALIGNMENTS

RESULT 1
AAR81323
ID AAR81323 standard; Protein; 123 AA.

AC AAR81323;

DT 02-APR-1996 (first entry)

XX Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.

XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.

XX Mus musculus.

XX W09519790-Al.

XX 27-JUL-1995.

XX 25-JAN-1995; 95WO-US01219.

XX 25-JAN-1994; 94US-0186269.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX Bendig MM, Jones TS, Leger OJ, Saldanha J;

XX WPI; 1995-269276/35.

XX New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 15.903 Seconds
(without alignments)
327.248 Million cell updates/sec

Title: US-09-155-739-11

Perfect score: 655

Sequence: 1 QVLVQSGAEVKKPEASVKV.....NGVYAMDYWGQGLVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
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- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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4	655	100.0	142	5	PCT-US95-01219-17
5	552	84.3	123	2	US-08-561-521-9
6	552	84.3	123	5	PCT-US95-01219-9
7	544	83.1	140	2	US-08-561-521-4
8	544	83.1	140	5	PCT-US95-01219-4
9	523.5	79.9	120	4	US-08-871-488A-19
10	523	79.8	117	3	US-08-646-265A-132
11	523	79.8	136	3	US-08-646-265A-99
12	523	79.8	269	3	US-08-646-265A-109
13	515	78.6	119	2	US-08-561-521-13
14	515	78.6	119	5	PCT-US95-01219-13
15	512	78.2	119	2	US-08-561-521-12
16	512	78.2	119	5	PCT-US95-01219-12
17	505	77.1	125	2	US-08-561-521-44
18	505	77.1	125	5	PCT-US95-01219-44
19	495	75.6	119	2	US-08-561-521-10
20	495	75.6	119	5	PCT-US95-01219-10
21	492	75.1	117	2	US-08-290-592E-17
22	492	75.1	117	5	PCT-US95-10053-14
23	492	75.1	117	5	PCT-US96-09448-17
24	492	75.1	119	4	US-09-438-954-41
25	491.5	75.0	118	2	US-08-232-081B-8
26	489.5	74.7	120	4	US-09-025-769B-36
27	489.5	74.7	120	4	US-09-025-769B-59

28	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
29	486	74.2	140	4	US-09-434-122-63	Sequence 63, Appl
30	484.5	74.0	135	1	US-08-137-117D-112	Sequence 112, App
31	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
32	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
33	484.5	74.0	139	2	US-08-452-164A-19	Sequence 19, Appl
34	484.5	74.0	139	3	US-08-603-024-18	Sequence 18, Appl
35	484.5	74.0	139	4	US-08-450-809-14	Sequence 14, Appl
36	481	73.4	121	1	US-08-202-047-23	Sequence 23, Appl
37	481	73.4	121	3	US-08-964-690-23	Sequence 23, Appl
38	480.5	73.4	124	4	US-09-301-593-16	Sequence 16, Appl
39	480.5	73.4	124	4	US-09-301-593-41	Sequence 41, Appl
40	475	72.5	119	4	US-09-438-954-4	Sequence 4, Appl
41	474	72.4	140	3	US-08-836-561-74	Sequence 74, Appl
42	474	72.4	140	4	US-09-434-122-74	Sequence 74, Appl
43	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
44	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
45	473	72.2	123	2	US-08-487-113D-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-11

Query Match 100.0%; Score 655; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGAEVKKPKGASVKYSCASGKFNKDTYIHWRQAPGQRLWMMGRIDPANGYTKY 60
DB 1 QVQLVQSGAEVKKPKGASVKYSCASGKFNKDTYIHWRQAPGQRLWMMGRIDPANGYTKY 60
QY 61 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 120
DB 61 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 120
QY 121 VSS 123
DB 121 VSS 123

RESULT 2

PCT-US95-01219-11
; Sequence 11, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saidanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VIA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-01219-11

Query Match 100.0%; Score 655; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 2.7e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QVQLVQSGAEVKKPKGASVKYSCASGKFNKDTYIHWRQAPGQRLWMMGRIDPANGYTKY 60
QY 61 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 120
DB 61 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 120
QY 121 VSS 123

DB 121 VSS 123
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RESULT 3

US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saidanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VIA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-17

Query Match 100.0%; Score 655; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 3.2e-58;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 120
DB 80 DPKFGQRTTITADTSASTAYMELSSLRSEDTAVYYCAREGYGNYGVYAMDYWGQGLT 139

QY 121 VSS 123
DB 140 VSS 142
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RESULT 4

PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 31.0606 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-11

Perfect score: 655

Sequence: 1 QVOLVQSGAEVKKPGASVKV.....NGVYAMDYWGQGLTVYSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:**

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	523.5	79.9	120	15	US-10-056-794-19
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6	523.5	79.8	136	11	US-09-749-873-99
7	523.5	79.8	269	11	US-09-749-873-109
8	492	75.1	117	10	US-09-158-120A-17
9	492	75.1	119	15	US-10-233-996-41
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18 479.5 73.2 252 11 US-09-880-748-1698
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41 468.5 71.5 249 11 US-09-880-748-1730
42 468 71.5 248 11 US-09-880-748-1178
43 467.5 71.4 245 11 US-09-880-748-1919
44 467 71.3 142 15 US-10-171-452A-2
45 466.5 71.2 126 11 US-09-791-153A-62
```

ALIGNMENTS

```
RESULT 1
US-10-056-794-19
; Sequence 19, Application US/10056794
; Publication No. US20030119078A1
; GENERAL INFORMATION:
; APPLICANT: Graves, Scott S.
; Reno John M.
; Mallett, Robert W.
; Hylarides, Mark D.
; Searle, Stephen M.J.
; Henry, Andrew H.
; Pedersen, Jan T.
; Rees, Anthony R.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
; ANTIGEN BOUND BY ANTIBODY NR-IJ-13 AND THEIR USE IN
; PRETARGETING METHODS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/056,794
; FILING DATE: 24-Jan-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey Ph.D., Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 690022.527C2
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-10-056-794-19

Query Match 79.9%; Score 523.5; DB 15; Length 120;
 Best Local Similarity 82.9%; Pred. No. 1.6e-45;
 Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKY 60
 DB 1 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKC 60
 QY 61 DPKFGQGVTTTADTSASTAYMELSLRSEDVAVYICAREGYGNYGVYANDYWGQGLVLT 120
 DB 61 DLSFGQGVTTTADTSINTAYMELSLRSDDTAVYICAREVLT---TGTWSLDYWGQGLVLT 117
 QY 121 VSS 123
 DB 118 VSS 120

RESULT 2
 US-10-244-821-4
 ; Sequence 4, Application US/10244821
 ; Publication No. US20030143233A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goshorn, Stephen Charles
 ; APPLICANT: Graves, Scott Stoll
 ; APPLICANT: Schultz, Joanne Elaine
 ; APPLICANT: Lin, Yukang
 ; APPLICANT: Sanderson, James Allen
 ; APPLICANT: Reno, John M.
 ; APPLICANT: Dearstynne, Erica A.
 ; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 ; FILE REFERENCE: 690022.547C3
 ; CURRENT APPLICATION NUMBER: US/10/244,821
 ; CURRENT FILING DATE: 2002-09-16
 ; NUMBER OF SEQ ID NOS: 92
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
 ; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-244-821-4

Query Match 79.9%; Score 523.5; DB 12; Length 431;
 Best Local Similarity 82.9%; Pred. No. 7e-45;
 Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKY 60
 DB 148 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKS 207
 QY 61 DPKFGQGVTTTADTSASTAYMELSLRSEDVAVYICAREGYGNYGVYANDYWGQGLVLT 120
 DB 208 DLSFGQGVTTTADTSINTAYMELSLRSDDTAVYICAREVLT---TGTWSLDYWGQGLVLT 264
 QY 121 VSS 123
 DB 265 VSS 267

RESULT 3
 US-10-013-173-4
 ; Sequence 4, Application US/10013173
 ; Publication No. US20030095977A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goshorn, Stephen C.
 ; APPLICANT: Graves, Scott Stoll
 ; APPLICANT: Schultz, Joanne Elaine
 ; APPLICANT: Lin, Yukang
 ; APPLICANT: Sanderson, James A.
 ; APPLICANT: Reno, John M.
 ; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 ; FILE REFERENCE: 690022.547C1
 ; CURRENT APPLICATION NUMBER: US/10/013,173
 ; CURRENT FILING DATE: 2001-12-07
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
 ; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-013-173-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;
 Best Local Similarity 82.9%; Pred. No. 7e-45;
 Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;
 QY 1 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKY 60
 DB 148 QVQLVQSGAEVKKPGASVKVSCKASGFKNDITYIHVVRQAPQGRLEWNGRIDPANGYTKS 207
 QY 61 DPKFGQGVTTTADTSASTAYMELSLRSEDVAVYICAREGYGNYGVYANDYWGQGLVLT 120
 DB 208 DLSFGQGVTTTADTSINTAYMELSLRSDDTAVYICAREVLT---TGTWSLDYWGQGLVLT 264
 QY 121 VSS 123
 DB 265 VSS 267

RESULT 4
 US-10-150-762-4
 ; Sequence 4, Application US/10150762
 ; Publication No. US20030103948A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goshorn, Stephen C.
 ; APPLICANT: Graves, Scott S.
 ; APPLICANT: Schultz, Joanne E.
 ; APPLICANT: Lin, Yukang
 ; APPLICANT: Sanderson, James A.
 ; APPLICANT: Reno, John M.
 ; APPLICANT: Dearstynne, Erica A.
 ; TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
 ; FILE REFERENCE: 690022.547C2
 ; CURRENT APPLICATION NUMBER: US/10/150,762
 ; CURRENT FILING DATE: 2002-05-17
 ; NUMBER OF SEQ ID NOS: 90
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Predicted amino acid sequence for huNR-LU-10
 ; OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.
 US-10-150-762-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:02:30 ; Search time 9.19394 Seconds
(without alignments)
629.141 Million cell updates/sec

Title: US-09-155-739-11

Perfect score: 655

Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYANDYWGQGLTVTVSS 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	427.5	65.3	147	1 HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1 HV03_MOUSE	P01747 mus musculus
3	408.5	62.4	139	1 HV07_MOUSE	P01751 mus musculus
4	405	61.8	117	1 HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1 HV02_MOUSE	P01746 mus musculus
6	396	60.5	117	1 HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1 HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1 HV13_MOUSE	P01757 mus musculus
9	375.5	57.3	118	1 HV51_MOUSE	P06330 mus musculus
10	373	56.9	117	1 HV12_MOUSE	P01756 mus musculus
11	371.5	56.7	137	1 HV11_MOUSE	P01755 mus musculus
12	369	56.3	138	1 HV48_MOUSE	P03980 mus musculus
13	364.5	55.6	120	1 HV50_MOUSE	P06329 mus musculus
14	360	55.0	121	1 HV01_MOUSE	P01745 mus musculus
15	360	55.0	136	1 HV15_MOUSE	P01759 mus musculus
16	355	54.2	125	1 HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1 HV1H_HUMAN	P08421 homo sapien
18	349	53.3	117	1 HV09_MOUSE	P01753 mus musculus
19	344.5	52.6	114	1 HV00_MOUSE	P01741 mus musculus
20	338	51.6	117	1 HV04_MOUSE	P01748 mus musculus
21	336	51.3	117	1 HV06_MOUSE	P01750 mus musculus
22	333.5	50.9	136	1 HV16_MOUSE	P01783 mus musculus
23	333	50.8	117	1 HV10_MOUSE	P01754 mus musculus
24	330.5	50.5	124	1 HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1 HV14_MOUSE	P01758 mus musculus
26	329	50.2	117	1 HV49_MOUSE	P06328 mus musculus
27	326	49.8	117	1 HV52_MOUSE	P06327 mus musculus
28	326	49.8	123	1 HV24_MOUSE	P01793 mus musculus
29	325.5	49.7	119	1 HV37_MOUSE	P01807 mus musculus
30	325.5	49.7	124	1 HV1D_HUMAN	P01760 homo sapien
31	324.5	49.5	119	1 HV38_MOUSE	P01808 mus musculus
32	323.5	49.4	119	1 HV40_MOUSE	P01810 mus musculus
33	320.5	48.9	122	1 HV3G_HUMAN	P01768 homo sapien

RESULT 1

HVIC_HUMAN STANDARD; PRT; 147 AA.

AC P01744; 21-JUL-1986 (Rel. 01, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig heavy chain V-I region ND precursor (Fragments).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=83065234; PubMed=6815656;

RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,

RA Bell L.O., Gould H.J.;

RT *Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.*;

RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).

RN [2]

RP SEQUENCE OF 20-147

RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;

RL (In) Bach M.K. (eds.);

RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,

RL Marcel Dekker, New York (1978).

CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

CC PROTEIN.

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSSP: P01789; IMCP.

DR GO: GO:0005576; C:extracellular; NAS.

DR GO: GO:0003823; F:antigen binding activity; NAS.

DR GO: GO:0006955; P:immune response; NAS.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS00835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 19

FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.

FT DOMAIN 20 131 IG-LIKE.

FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.

FT DISULFID 41 115

FT CONFLICT 21 21 T -> V (IN REF. 2).

FT CONFLICT 53 54 IH -> HI (IN REF. 2).

FT CONFLICT 67 68 VG -> GV (IN REF. 2).

FT CONFLICT 125 125 MISSING (IN REF. 2).

FT NON_TER 147 147

SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 147;

Best Local Similarity 64.1%; Pred. No. 1-le-36;

Matches 82; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

34 319 48.7 117 1 HV42_MOUSE P01812 mus musculus
35 318.5 48.6 122 1 HV3A_HUMAN P01762 homo sapien
36 318 48.5 121 1 HV3J_HUMAN P01771 homo sapien
37 317 48.4 123 1 HV19_MOUSE P01788 mus musculus
38 315 48.1 123 1 HV18_MOUSE P01787 mus musculus
39 314.5 48.0 122 1 HV21_MOUSE P01790 mus musculus
40 314 47.9 117 1 HV05_MOUSE P01749 mus musculus
41 313 47.8 123 1 HV25_MOUSE P01794 mus musculus
42 313 47.8 142 1 HV01_RAT P01805 rattus norv
43 312 47.6 118 1 HV39_MOUSE P01809 mus musculus
44 312 47.6 123 1 HV22_MOUSE P01791 mus musculus
45 311.5 47.6 122 1 HV3H_HUMAN P01769 homo sapien

ALIGNMENTS


```

1 EVQLVESGAELVKPGASVKYSCKASGTFTSSYYMHVRQAPGQGLEWMGIIINPSGGSITSY 60
Ddb
61 DPKFGQGRVITADPSASTAYMELSSLASEDTATYYCAREGYTNGYVYAM-----DY 112
Qy
61 AQKFGQGRVTMDTSTVYMELSSLASEDTATYYCAR-----GLYVVVPAAFSRFDY 113
Ddb
113 WQGGTLTVTSS 123
Qy
114 WQGGTLTVTSS 124
Ddb

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RESULT 2	Q96QSO	PRELIMINARY;	PRT;	159 AA.
ID	Q96QSO			
AC	Q96QSO;			
DT	01-DEC-2001 (TREMBlurel. 19, Created)			
DT	01-DEC-2001 (TREMBlurel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBlurel. 23, Last annotation update)			
DT	Putative matrix cell adhesion molecule-3.			
DE	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

```

RESULT 3
Q99L31
ID ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR

```

```

DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS08335; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
DR SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match          67.2%; Score 440; DB 11; Length 468;
Best Local Similarity 67.5%; Pred. No. 2.8e-38;
Matches 83; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

QY      1 QVLVQSGAEVKKPGASVKYSCKASGFNKTDTIHWVQAPQRIEWGRIDDPANGYTKY 60
         :|||: |||: :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      20 EVQLQSGAEVLRPGASVKLSCTASGFNIDLSMHVVKORPEGLIEWIGVIDPETGKY 79

QY      61 DPKFGRTVITADTSASTAYWEISSLRSEDTAVYICAREGYGNGTVYAMDYWGQGLTVT 120
         :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db      80 APKQDKATITADTSSTAYWLQLSSLTSEDTAVYICARNLLTGGY----YDWGQGLTIT 135

QY      121 VSS 123
         |||
Db      136 VSS 138

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RESULT 4	Q9JL85	PRELIMINARY;	PRT;	109 AA.
ID	Q9JL85			
AC	Q9JL85;			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Anti-myosin immunoglobulin heavy chain variable region (fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c;			
RX	MEDLINE=20448942; PubMed=10992488;			
RA	Malkiel S., Liao L., Cunningham M.W., Diamond B.;			
RT	T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin*.			
RL	Infect. Immun. 68:5803-5808(2000).			
EMBL	AF206021; AAF69319.1; -.			
DR	HSSP; P01810; 2FBU.			
DR	InterPro: IPR007110; Ig-LIKE.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_v.			
DR	Pfam: PF000047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
FT	NON_TER	1		
FT	NON_TER	109		
FT	NON_TER	109		
SO	SEQUENCE	109 AA;	11944 MW;	DFE615FE6CED4EDE CRC64:

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Query Match      66.0%; Score 432; DB 11; Length 109;
Best Local Similarity 68.7%; Pred. No. 3.2e-38;
Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1
QY      9  AEVKKPGASVKSKASGFNTKDYIHWVQAQGLRLEMMGRIDTPANGYTKYDKPKQGRV 68
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db      1  AELVPGASVLKCTAGSFNTEDYMEHWKQRPQGLEIGRIDTPATGSHKYDKPKQGA 60
QY     69  TTATDTSASTAYMELLSLRSDTAYVYCAREGYNGVGYVANDYWGQGLTVTSS 123
      ||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db     61  TTTSPTSGNTAYQLSLTSDTAYVYCVRR-----GAVFYWGQGLTAVSS 109

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 16.2909 Seconds
(without alignments)
327.248 Million cell updates/sec

Title: US-09-155-739-2

Perfect score: 680

Sequence: 1 MRPSIQFLGILLFWLHGAQC.....YCIQYDNLWTFGGTGKLEIK 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	680	100.0	126	2	US-08-561-521-2
2	680	100.0	126	2	US-08-561-521-15
3	680	100.0	126	5	PCT-US95-01219-2
4	680	100.0	126	5	PCT-US95-01219-15
5	634	93.2	128	1	US-08-339-582-4
6	569	83.7	106	2	US-08-561-521-5
7	569	83.7	106	5	PCT-US95-01219-5
8	539	78.3	359	4	US-09-646-028-16
9	539	79.3	361	4	US-09-646-028-13
10	535	78.7	374	4	US-09-646-028-15
11	510.5	75.1	107	2	US-08-888-366-22
12	508	74.7	106	2	US-08-561-521-7
13	508	74.7	106	5	PCT-US95-01219-7
14	508	74.7	637	1	US-08-235-838-16
15	508	74.7	637	2	US-08-465-473B-16
16	503	74.0	241	1	US-08-235-838-11
17	503	74.0	241	2	US-08-465-473B-11
18	501	73.7	355	3	US-08-875-811-57
19	438.5	64.5	128	1	US-08-259-372A-14
20	438.5	64.5	128	1	US-08-468-671-14
21	437.5	64.3	127	1	US-08-458-516-5
22	437.5	64.3	127	3	US-08-348-548-4
23	437.5	64.3	127	5	PCT-US95-15716-4
24	437.5	64.3	131	1	US-08-236-520-2
25	437.5	64.3	131	5	PCT-US95-05262-2
26	435.5	64.0	234	4	US-09-740-002-24
27	434.5	63.9	128	4	US-09-225-322B-10

Sequence 19, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 63, Appl
Sequence 63, Appl
Sequence 71, Appl
Sequence 2, Appl
Sequence 37, Appl
Sequence 17, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 7, Appl
Sequence 6, Appl

US-09-225-322B-19
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US-09-764-304-19
US-08-480-434-63
US-08-053-451B-63
US-08-836-561-71
US-09-434-122-71
US-08-217-918-2
US-08-137-117D-37
US-08-436-717-37
US-08-649-100-17
US-08-157-101A-5
US-08-579-940-2
US-08-838-692-4
US-08-137-117D-29
US-08-436-717-29
US-08-933-983-7
US-08-621-751A-6

ALIGNMENTS

RESULT 1

US-08-561-521-2

; Sequence 2, Application US/08561521

; Patent No. 5840299

; GENERAL INFORMATION:

; APPLICANT: Bendig, Mary M.

; APPLICANT: Leger, Olivier J.

; APPLICANT: Saldanha, Jose

; APPLICANT: Jones, S. Tarran

; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

; TITLE OF INVENTION: Adhesion Molecule VIA-4

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/561,521

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/186,269A

; FILING DATE: 25-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William L.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15270-14

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-543-9600

; TELEFAX: 415-543-5043

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 126 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-561-521-2

Query Match 100.0%; Score 680; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 2,1e-59;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60
 Db |||||||
 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60
 QY 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120
 Db |||||||
 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120

QY 121 TKLEIK 126
 Db |||||||

QY 121 TKLEIK 126
 Db |||||||

RESULT 2

US-08-561-521-15
 ; Sequence 15, Application US/08561521
 ; Patent No. 5840299
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; TITLE OF INVENTION: Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,269A
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-561-521-15

Query Match 100.0%; Score 680; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.le-59;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60
 Db |||||||
 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60
 QY 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120
 Db |||||||
 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120
 QY 121 TKLEIK 126
 Db |||||||

RESULT 4
 PCT-US95-01219-15
 ; Sequence 15, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran

Db 121 TKLEIK 126

RESULT 3

PCT-US95-01219-2
 ; Sequence 2, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; TITLE OF INVENTION: Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01219
 ; FILING DATE: 25-JAN-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/186,269
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-01219-2

Query Match 100.0%; Score 680; DB 5; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.le-59;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60
 Db |||||||
 1 MRPSIQFLGLLFWLHGAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYMWYQHKP 60

QY 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120
 Db |||||||
 61 GKRPRLLIHYTSALQGPISRFSGSGGRDYSFNISNLEPEDIAITYYCLOYDNLWTFGGG 120

QY 121 TKLEIK 126
 Db |||||||

QY 121 TKLEIK 126
 Db |||||||

RESULT 4

PCT-US95-01219-15
 ; Sequence 15, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 31.8182 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-2

Perfect score: 680

Sequence: 1 MRPSIQFLGLLFWLHGAQC.....YCLQYDNLWTFGGTKLEIK 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2.6/ptodata/1/pubpaa/US07_PUBCOMB.pap.*
- 2: /cgn2.6/ptodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
- 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
- 5: /cgn2.6/ptodata/1/pubpaa/US07_NEW_PUB.pap.*
- 6: /cgn2.6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pap.*
- 7: /cgn2.6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
- 8: /cgn2.6/ptodata/1/pubpaa/US08_PUBCOMB.pap.*
- 9: /cgn2.6/ptodata/1/pubpaa/US09A_PUBCOMB.pap.*
- 10: /cgn2.6/ptodata/1/pubpaa/US09B_PUBCOMB.pap.*
- 11: /cgn2.6/ptodata/1/pubpaa/US09C_PUBCOMB.pap.*
- 12: /cgn2.6/ptodata/1/pubpaa/US09_NEW_PUB.pap.*
- 13: /cgn2.6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
- 14: /cgn2.6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
- 15: /cgn2.6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
- 16: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pap.*
- 17: /cgn2.6/ptodata/1/pubpaa/US60_NEW_PUB.pap.*
- 18: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	539	79.3	359	12	US-10-335-394-16
2	539	79.3	361	12	US-10-335-394-13
3	535	78.7	374	12	US-10-335-394-15
4	490	72.1	109	9	US-09-229-200A-7
5	482.5	71.0	108	9	US-09-229-200A-17
6	481.5	70.8	131	15	US-10-207-655-256
7	481.5	70.8	266	15	US-10-207-655-260
8	481.5	70.8	550	15	US-10-207-655-270
9	445.5	65.5	127	12	US-10-268-883-5
10	442.5	65.1	236	10	US-09-859-053-30
11	441	64.9	241	15	US-10-221-945-1
12	437.5	64.3	131	8	US-08-779-784-21
13	435.5	64.0	234	9	US-09-740-002-24
14	434.5	63.9	128	9	US-09-764-304-10
15	434.5	63.9	128	9	US-09-764-304-19

16	434.5	63.9	128	12	US-10-166-626-10	Sequence 10, Appl
17	434.5	63.9	128	12	US-10-166-626-19	Sequence 19, Appl
18	434.5	63.9	128	15	US-10-265-713-10	Sequence 10, Appl
19	434.5	63.9	128	15	US-10-265-713-19	Sequence 19, Appl
20	431.5	63.5	108	9	US-09-229-200A-11	Sequence 11, Appl
21	431.5	63.5	108	9	US-09-229-200A-15	Sequence 15, Appl
22	431.5	63.5	108	9	US-09-229-200A-16	Sequence 16, Appl
23	429.5	63.2	127	15	US-10-283-349-71	Sequence 71, Appl
24	424.5	62.4	127	15	US-10-084-139-2	Sequence 2, Appl
25	424.5	62.4	259	12	US-10-053-530-13	Sequence 13, Appl
26	424.5	62.4	259	15	US-10-207-655-13	Sequence 13, Appl
27	420.5	61.8	234	9	US-09-800-729-150	Sequence 150, Appl
28	418.5	61.5	142	9	US-09-797-481-2	Sequence 2, Appl
29	418.5	61.5	142	9	US-09-844-736-4	Sequence 4, Appl
30	418.5	61.5	142	15	US-10-162-396-4	Sequence 4, Appl
31	417.5	61.4	127	11	US-09-977-283A-7	Sequence 7, Appl
32	416.5	61.3	127	15	US-10-283-349-88	Sequence 88, Appl
33	416	61.2	234	9	US-09-740-002-26	Sequence 26, Appl
34	414.5	61.0	128	9	US-09-855-271-26	Sequence 26, Appl
35	413.5	60.8	125	10	US-09-809-739-1	Sequence 1, Appl
36	413.5	60.8	127	15	US-10-084-139-6	Sequence 6, Appl
37	413	60.7	237	9	US-09-056-160B-100	Sequence 100, Appl
38	413	60.7	491	14	US-10-011-125-2	Sequence 2, Appl
39	412.5	60.7	127	12	US-10-289-181-8	Sequence 8, Appl
40	411.5	60.5	108	9	US-09-905-243-73	Sequence 73, Appl
41	410.5	60.4	107	12	US-10-330-613-26	Sequence 26, Appl
42	410.5	60.4	107	12	US-10-330-530-26	Sequence 26, Appl
43	410.5	60.4	127	11	US-09-977-283A-17	Sequence 17, Appl
44	409.5	60.2	127	15	US-10-283-349-92	Sequence 92, Appl
45	407.5	59.9	107	9	US-09-056-160B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-335-394-16
; Sequence 16, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: KwaK, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct
US-10-335-394-16

Query Match 79.3%; Score 539; DB 12; Length 359;
Best Local Similarity 91.8%; Pred. No. 6.2e-42;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 17 GAQCDIQMTQSPSSLSASLGKVTITCKTSQDINKYNAWYOHKPKRPRLLIHYTSALQP 76
Db 229 GSGSDIQMTQSPSSLSASLGKVTITCKASQDINKYNAWYOHKPKRPRLLIHYTSLQP 288
QY 77 GIPSRFSGSGGRDYSFNSINLEPEDIATYCYLQYDNLWTFGGTKLEIK 126
Db 289 GIPSRFSGSGGRDYSFNSINLEPEDIATYCYLQYDNLWTFGGTKLEIK 338

RESULT 2
 US-10-335-394-13
 ; Sequence 13, Application US/10335394
 ; Publication No. US20030138452A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kwak, Larry
 ; APPLICANT: Biragyn, Arya
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
 ; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
 ; FILE REFERENCE: 14014.0316/P
 ; CURRENT APPLICATION NUMBER: US/10/335,394
 ; CURRENT FILING DATE: 2002-12-31
 ; PRIOR APPLICATION NUMBER: US/09/646,028
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: 60/077,745
 ; PRIOR FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 13
 ; LENGTH: 361
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
 US-10-335-394-13

Query Match 79.3%; Score 539; DB 12; Length 361;
 Best Local Similarity 91.8%; Pred. No. 6.2e-42;
 Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 17 GAQCDIQWQSPSSLSASLGKVTITCKTSQDINKYMAWYQHKPRPRLIIHYTSLQ 76
 DB 231 GSGSDIQWQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRPRLIIHYTSLQ 290
 QY 77 GIPRFGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 126
 DB 291 GIPRFGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 340

RESULT 3
 US-10-335-394-15
 ; Sequence 15, Application US/10335394
 ; Publication No. US20030138452A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kwak, Larry
 ; APPLICANT: Biragyn, Arya
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
 ; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
 ; FILE REFERENCE: 14014.0316/P
 ; CURRENT APPLICATION NUMBER: US/10/335,394
 ; CURRENT FILING DATE: 2002-12-31
 ; PRIOR APPLICATION NUMBER: US/09/646,028
 ; PRIOR FILING DATE: 2000-09-12
 ; PRIOR APPLICATION NUMBER: 60/077,745
 ; PRIOR FILING DATE: 1998-03-12
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
 US-10-335-394-15

Query Match 78.7%; Score 535; DB 12; Length 374;
 Best Local Similarity 94.3%; Pred. No. 1.5e-41;
 Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 21 DIQWQSPSSLSASLGKVTITCKTSQDINKYMAWYQHKPRPRLIIHYTSLQ 80
 DB 95 DIQWQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRPRLIIHYTSLQ 154

QY 81 RFSGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 126
 DB 155 RFSGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 200
 RESULT 4
 US-09-229-200A-7
 ; Sequence 7, Application US/09229200A
 ; Patent No. US20020099179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jolliffe et al.
 ; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Johnson & Johnson
 ; STREET: One Johnson & Johnson Plaza
 ; CITY: New Brunswick
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08933-7003
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: <Unknown>
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/229,200A
 ; FILING DATE: 13-Jan-1999
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: John W. Wallen, III
 ; REGISTRATION NUMBER: 35,403
 ; REFERENCE/DOCKET NUMBER: ORT-948
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (858) 784-3239
 ; TELEFAX: (908) 524-2808
 ; INFORMATION FOR SEQ ID NO: 7:
 ; LENGTH: 109
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-229-200A-7

Query Match 72.1%; Score 490; DB 9; Length 109;
 Best Local Similarity 86.1%; Pred. No. 5.6e-38;
 Matches 93; Conservative 8; Mismatches 5; Indels 2; Gaps 1;
 QY 21 DIQWQSPSSLSASLGKVTITCKTSQDINKYMAWYQHKPRPRLIIHYTSLQ 80
 DB 1 DIQWQSPSSLSASLGKVTIACKASQDINNYIAWYQHKPGKPRPRLIIHYTSLQ 60
 QY 81 RFSGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 126
 DB 61 RFSGSGSGRDYSFNISNLEPEDIATYICLYQDNLMTFTGGGKLEIK 108
 RESULT 5
 US-09-229-200A-17
 ; Sequence 17, Application US/09229200A
 ; Patent No. US20020099179A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jolliffe et al.
 ; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Johnson & Johnson
 ; STREET: One Johnson & Johnson Plaza
 ; CITY: New Brunswick
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08933-7003

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:09:40 ; Search time 17,8182 Seconds
(without alignments)
680.050 Million cell updates/sec

Title: US-09-155-739-2

Perfect score: 680

Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGKLEIK 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	589	86.6	125	2 S03365	Ig kappa chain - m
2	535	78.7	104	2 S26330	Ig kappa chain v r
3	526	77.4	104	2 S26329	Ig kappa chain v r
4	524	77.1	106	2 C33936	Ig kappa chain v r
5	490.5	72.1	129	2 S52789	Ig kappa chain v r
6	490.5	72.1	103	2 S26332	Ig light chain v r
7	488	71.8	97	2 PH1064	Ig light chain v r
8	476	70.0	94	2 E33730	Ig kappa chain v r
9	471.5	69.3	107	2 PL0270	Ig kappa chain v r
10	465.5	68.5	107	2 PL0272	Ig kappa chain v r
11	464.5	68.3	107	2 PL0269	Ig kappa chain v r
12	464.5	68.3	107	2 PL0271	Ig kappa chain v r
13	453.5	66.7	127	2 S40367	Ig kappa chain v-J
14	445.5	65.5	132	2 S40334	Ig kappa chain - h
15	444.5	65.4	139	2 S40365	Ig kappa chain - h
16	443.5	65.2	129	2 S40317	Ig kappa chain - h
17	442.5	65.1	125	2 S40333	Ig kappa chain v-J
18	442.5	65.1	131	2 S40352	Ig kappa chain v-J
19	441.5	64.9	129	1 KLH0WK	Ig kappa chain pre
20	439.5	64.6	94	2 PH1063	Ig light chain v r
21	439	64.6	124	2 S40336	Ig kappa chain v-J
22	438.5	64.5	123	2 S40331	Ig kappa chain - h
23	438	64.4	117	2 S42263	Ig kappa chain v r
24	437.5	64.3	122	2 A29380	Ig kappa chain pre
25	437.5	64.3	127	2 S52447	Ig kappa chain v r
26	437.5	64.3	135	2 S24320	Ig kappa chain pre
27	436.5	64.2	128	2 PL0101	Ig kappa chain pre
28	436.5	64.2	129	2 S52793	Ig kappa chain v r
29	435.5	64.0	127	2 S04574	Ig kappa chain pre

30 435.5 64.0 127 2 S11240 Ig kappa chain v r
31 434.5 63.9 141 2 A49134 Ig kappa chain v-l
32 433.5 63.7 126 2 A34504 Ig kappa chain pre
33 433.5 63.7 234 2 S14237 Ig kappa chain v r
34 432 63.5 117 2 S43528 Ig kappa chain v r
35 430.5 63.3 127 2 PH1224 Ig kappa chain pre
36 428.5 63.0 125 2 S40316 Ig kappa chain - h
37 427.5 62.9 129 2 S52792 Ig kappa chain v r
38 426.5 62.7 125 2 S40350 Ig kappa chain - h
39 425.5 62.6 128 2 S40349 Ig kappa chain v-J
40 425.5 62.6 123 1 KVMST1 Ig kappa chain pre
41 422.5 62.1 124 2 S40348 Ig kappa chain - h
42 419.5 61.7 122 2 S40314 Ig kappa chain v-J
43 419.5 61.7 124 2 S03521 Ig kappa chain pre
44 418 61.5 127 2 A23986 Ig kappa chain pre
45 416.5 61.3 85 2 F36025 Ig light chain v r

ALIGNMENTS

RESULT 1

S09365

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S09365

R:Feddersen, R.; van Ness, B.

Nucleic Acids Res. 17, 9797-9809, 1989

A:Title: Direct evidence for intrastand DNA inversion of kappa immunoglobulin gene

A:Reference number: S09365; MUID:90098844; PMID:2513557

A:Accession: S09365

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-125 <FED>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 589; DB 2; Length 125;
Best Local Similarity 90.6%; Pred. No. 6.le-44;
Matches 115; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 1 MRPSIQFLGLLLFWLHGAQCIDIQTSPSSLSASLGKVTITCKTSODINKYAWYQHKP 60

Db 1 MRPSIQFLGLLLFWLHGAQCIDIQTSPSSLSASLGKVTITCKTSODINKYAWYQHKP 57

QY 61 GKRPRLTHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDATYCYLDNLW-TFGG 119

Db 58 GKRPRLTHYTSALQPGIPSRFSGSGSRDYSFNISNLEPEDATYCYLDNLW-TFGG 117

QY 120 GTKLEIK 126

Db 118 GTKLEIK 124

RESULT 2

S26330

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26330

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a prote

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26330

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

A:Cross-references: EMBL:X59185; NID:952316; PIDN:CAA41895.1; PID:91334063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 535; DB 2; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.3e-39;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 80
|||||
DB 1 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 60
|||||

QY 81 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLE 124
|||||
DB 61 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLE 104
|||||

RESULT 3

S26329

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26329

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein e

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26329

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

C:Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 526; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.3e-38;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 80
|||||
DB 1 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 60
|||||

QY 81 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLE 124
|||||
DB 61 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLE 104
|||||

RESULT 4

C33936

Ig kappa chain V region (VM113) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C:Accession: C33936

R:Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989

A:Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene

A:Reference number: A33936; MUID:89282831; PMID:2471975

A:Accession: C33936

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-106 <MEE>

C:Cross-references: GB:J04577; NID:g623187; PIDN:AA660443.1; PID:g623189

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 524; DB 2; Length 106;
Best Local Similarity 91.5%; Pred. No. 2e-38;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 80
|||||
DB 1-DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 60
|||||

QY 81 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLEIK 126
|||||
DB 61 RFGSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGGGKLEIK 106
|||||

RESULT 5

S52789

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C:Accession: S52789

R:Rocca, A.; Khamilchi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; De;

submitted to the EMBL Data Library, March 1995

A:Description: Light chain V region gene usage restriction and peculiarities in myel

A:Reference number: S52789

A:Accession: S52789

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-129 <ROC>

C:Cross-references: EMBL:X85985; NID:g758588; PIDN:CAA59987.1; PID:g758589

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 490.5; DB 2; Length 129;
Best Local Similarity 72.4%; Pred. No. 1.9e-35;
Matches 92; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

QY 1 MRPSIQFLGLLFWLHGAQCIDQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKP 60
|||||
DB 3 MRVPAQLGLLGLLWLSGARCDIQMTQSPSSLSASVGDRTTTCQASQDISNLYWYQKQP 62
|||||

QY 61 GRPRLIIHYTSALQPGIPSRFSGSGRDYSFNISNLEPEDIATYYCLOYDNLWTFGG 119
|||||
DB 63 GRAPKLLIIHAASSLETGVPFRFSGSGGTDFSTISSLPEDLATYYCQYDNLPLTFGG 122
|||||

QY 120 GTKLEIK 126
|||||
DB 123 GTKVEIK 129
|||||

RESULT 6

S26332

Ig light chain V region - mouse (fragment)

N:Alternate names: Ig kappa chain V region

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000

C:Accession: S26332; S26331

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26332

A:Molecule type: mRNA

A:Residues: 1-103 <STA>

C:Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064

A:Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are

A:Accession: S26331

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-103 <ST2>

C:Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 490; DB 2; Length 103;
Best Local Similarity 87.4%; Pred. No. 1.7e-35;
Matches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 21 DIQMTQSPSSLSASLGKVTITCKTSQDINKYMAVYQHKPKRPRLLIHYTSALQPGIPS 80
|||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:02:30 ; Search time 9.41818 seconds
(without alignments)
629.141 Million cell updates/sec

Title: US-09-155-739-2

Perfect score: 680

Sequence: 1 MRPSIQFLGLLFWLHGAQC.....YCLQYDNLWTFGGTKLEIK 126

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441.5	64.9	129	1 KV1L_HUMAN	P04431 homo sapien
2	425.5	62.6	128	1 KV5D_MOUSE	P01637 mus musculus
3	412.5	60.7	129	1 KV1X_HUMAN	P04432 homo sapien
4	402	59.1	117	1 KV1J_HUMAN	P01602 homo sapien
5	400	58.8	115	1 KV5P_MOUSE	P01638 mus musculus
6	397.5	58.5	108	1 KV1B_HUMAN	P01594 homo sapien
7	395.5	58.2	108	1 KV1O_HUMAN	P01607 homo sapien
8	392.5	57.7	108	1 KV1P_HUMAN	P01608 homo sapien
9	389.5	57.3	108	1 KV1Y_HUMAN	P80362 homo sapien
10	380.5	56.0	108	1 KV1A_HUMAN	P01593 homo sapien
11	379.5	55.8	108	1 KV1M_HUMAN	P01605 homo sapien
12	378.5	55.7	130	1 KV5Q_MOUSE	P01639 mus musculus
13	378.5	55.7	133	1 KV4B_HUMAN	P06313 homo sapien
14	378	55.6	117	1 KV1I_HUMAN	P01601 homo sapien
15	377.5	55.5	108	1 KV5J_MOUSE	P01643 mus musculus
16	377	55.4	107	1 KV1D_HUMAN	P01596 homo sapien
17	375	55.1	134	1 KV4C_HUMAN	P06314 homo sapien
18	374.5	55.1	108	1 KV5O_MOUSE	P01648 mus musculus
19	373.5	54.9	108	1 KV1Q_HUMAN	P01609 homo sapien
20	373.5	54.9	108	1 KV5N_MOUSE	P01647 mus musculus
21	371.5	54.6	108	1 KV5K_MOUSE	P01644 mus musculus
22	369.5	54.3	108	1 KV5M_MOUSE	P01645 mus musculus
23	368.5	54.2	108	1 KV5L_MOUSE	P01610 homo sapien
24	366.5	53.9	108	1 KV1R_HUMAN	P01595 homo sapien
25	362.5	53.3	108	1 KV1C_HUMAN	P01606 homo sapien
26	360.5	53.0	108	1 KV1H_HUMAN	P01600 homo sapien
27	359.5	52.9	108	1 KV1N_HUMAN	P01606 homo sapien
28	357.5	52.6	108	1 KV1E_HUMAN	P01597 homo sapien
29	357.5	52.6	108	1 KV1V_HUMAN	P04430 homo sapien
30	355.5	52.3	108	1 KV1F_HUMAN	P01598 homo sapien
31	354.5	52.1	108	1 KV1S_HUMAN	P01611 homo sapien
32	353.5	52.0	115	1 KV5C_MOUSE	P01635 mus musculus
33	352.5	51.8	108	1 KV1K_HUMAN	P01603 homo sapien

ALIGNMENTS

RESULT 1

ID	KV1W_HUMAN	STANDARD;	PRT;	129 AA.
AC	P04431;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	19 kappa chain V-I region Walker precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85014148; PubMed=5091049;			
RA	Klobeck H.G., Combratio G., Zachau H.G.;			
RT	"Immunoglobulin genes of the kappa light chain type from two human			
RT	lymphoid cell lines are closely related.";			
RL	Nucleic Acids Res. 12:6995-7006(1984).			

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EMBL; X00965; CAA25477.1; ALT_TERM.
PIR; A01883; K1HOWK.
HSSP; P01607; IREI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 22
CHAIN 1 22
IG KAPPA CHAIN V-I REGION WALKER.
DOMAIN 23 129
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
DOMAIN 46 56
FRAMEWORK-2.
DOMAIN 57 71
COMPLEMENTARITY-DETERMINING-2.
DOMAIN 72 78
FRAMEWORK-3.
DOMAIN 79 110
COMPLEMENTARITY-DETERMINING-3.
DOMAIN 111 119
FRAMEWORK-4.
DOMAIN 120 129
DISULFID 45 110
BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match

64.9%; Score 441.5; DB 1; Length 129;

Best Local Similarity

66.9%; Pred. No. 1.7e-38;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:01:50 ; Search time 61.0909 Seconds
(without alignments)
363.748 Million cell updates/sec

Title: US-09-155-739-4

Perfect score: 746

Sequence: 1 MKCSVMFFLMAVTVGNSE.....YGNVGVYAMDYWGQTSVTV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

1:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	746	100.0	140	16 AAR81327	Mouse VLA-4 antibo
2	746	100.0	140	18 AAW22410	Alpha-4 integrin m
3	645	86.5	123	16 AAR81330	Mouse anti-VLA-4 a
4	633	84.9	136	17 AAW04379	Chimeric human/mu
5	629	84.3	140	12 AAR11384	Variable gamma hea
6	625	83.8	136	16 AAR76664	Murine ONS-21 anti
7	595	79.8	136	14 AAR41679	V heavy chain of r
8	593.5	79.6	137	18 AAW21845	Heavy chain variab
9	591	79.2	138	19 AAW63828	Human Mab #117-10C

10	584	78.3	142	16 AAR81333	Human VLA-4 reshap
11	584	78.3	142	18 AAW22428	humanised alpha-4
12	576.5	77.3	135	21 AAR07967	Amino acid sequenc
13	570.5	76.5	137	17 AAR95948	HNK-20 variable he
14	544	72.9	123	16 AAR81323	Humanized VLA-4 an
15	539.5	72.3	135	21 AAB07969	A heavy chain vari
16	537	72.0	123	18 AAW22413	Humanised alpha-4
17	535.5	71.8	437	19 AAW37738	Nucleotide sequenc
18	527	70.6	119	24 ABP97650	Amino acid sequenc
19	524.5	70.3	122	21 AAF33590	Heavy chain from a
20	521.5	69.9	120	14 AAR30767	Heavy chain variab
21	521.5	69.9	120	19 AAW44121	Heavy chain variab
22	521.5	69.9	120	23 AAU79031	Mouse antibody NR-
23	518.5	69.5	113	15 AAR60527	Heavy chain variab
24	517	69.3	143	15 AAR59942	Anti-VLA4 rab huma
25	516.5	69.2	120	16 AAR79889	Anti-EGFR antibody
26	516.5	69.2	150	24 AAE33371	Hybridoma 902 immu
27	516	69.2	121	20 AAW96741	Heavy chain variab
28	516	69.2	121	24 AAB08538	Mouse anti-VLA-4 a
29	513	68.8	121	20 AAW96744	Heavy chain variab
30	513	68.8	121	24 ABU08543	Mouse anti-VLA-4 a
31	513	68.8	138	22 AAG66455	VEGF SCFv protein
32	511	68.5	120	14 AAR39817	HPL/2 Vh. Homo sa
33	511	68.5	120	15 AAR53749	Anti-VLA4 Ab HPL/2
34	511	68.5	120	20 AAY23984	Antibody HPL/2 hea
35	511	68.5	120	22 AAB73462	Murine anti-VLA-4
36	509.5	68.3	126	12 AAR15439	Heavy chain variab
37	509.5	68.3	120	14 AAR39566	Sequence of the va
38	508	68.1	120	14 AAR75617	Anti-RANK ligand m
39	507.5	68.0	133	23 AAB56873	MAB CT-M-01 heavy
40	505.5	67.8	138	21 AAY56873	Anti-HMFG MAB CTMO
41	505.5	67.8	139	18 AAW29750	Murine anti-botuli
42	504	67.6	254	20 AAY30117	Murine anti-botuli
43	504	67.6	254	20 AAY30119	Murine anti-botuli
44	504	67.6	254	20 AAY30121	Murine anti-botuli
45	504	67.6	254	20 AAY30123	Murine anti-botuli

ALIGNMENTS

RESULT 1

AAR81327

ID AAR81327 standard; Protein; 140 AA.

XX AAR81327;

AC AAR81327;

XX 23-MAR-1996 (first entry)

DE Mouse VLA-4 antibody 21.6 light heavy variable region.

XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

KW antibody engineering.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Region /note= "signal peptide"

FT Region 20..49 "framework region 1"

FT Region /note= "framework region 1"

FT Region /note= "complementarity determining region 1"

FT Region /note= "framework region 2"

FT Region /note= "complementarity determining region 2"

FT Region /note= "framework region 3"

FT Region /note= "complementarity determining region 3"

FT Region /note= "framework region 4"

XX WO9519790-A1.
 XX 27-JUL-1995.
 XX 25-JAN-1995; 95WO-US01219.
 XX 25-JAN-1994; 94US-0186269.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 XX Bendig MM, Jones TS, Leger OJ, Saldanha J;
 XX WPI; 1995-269276/35.
 XX N-PSDB; AAQ99892.
 XX New humanised antibodies against VIA-4 - used for inhibiting
 PT leukocyte adhesion to endothelial cells, partic. for treating
 PT inflammatory disease.
 XX Disclosure; Fig 2; 105pp; English.
 XX The sequence represents the mouse antibody 21.6 heavy chain variable
 CC region directed against leukocyte adhesion molecule VIA-4. Cloned
 CC cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
 CC linked to human constant regions in the construction of a humanized
 CC antibody against VIA-4. The 5' and 3' ends of the mouse cDNAs are
 CC modified using PCR primers (see AAQ99895-98) and then subcloned into
 CC mammalian cell expression vectors containing human kappa or gamma-1
 CC constant regions. In the humanized heavy chain, amino acids H27,
 CC H28, H29, H30, H44 and H71 in the human HC VR framework are replaced
 CC by the amino acid present in the equivalent position of the mouse
 CC 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are
 CC transfected into COS cells. The humanized antibodies can be used
 CC to inhibit adhesion of a leukocyte to an endothelial cell and
 CC to treat inflammatory diseases such as multiple sclerosis. They
 CC can also be used in the treatment of stroke, cerebral trauma,
 CC meningitis or encephalitis. The antibodies can also be used for
 CC detecting VIA-4, for affinity purification or for generating
 CC anti-idiotypic antibodies.
 XX Sequence 140 AA;
 XX Query Match 100.0%; Score 746; DB 16; Length 140;
 XX Best Local Similarity 100.0%; Pred. No. 1e-59;
 XX Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKCSWYFFLMVAVTVGVNSEVQLQSGAEIVKPGASVKLSCTASGFNKTIDYIHCVKQRP 60
 Db 1 MKCSWYFFLMVAVTVGVNSEVQLQSGAEIVKPGASVKLSCTASGFNKTIDYIHCVKQRP 60
 QY 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSSLTSEDYVFCAREGY 120
 Db 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSSLTSEDYVFCAREGY 120
 QY 121 YGNYGYVAMDYWGQGSVTV 140
 Db 121 YGNYGYVAMDYWGQGSVTV 140
 RESULT 2
 ID AAW22410
 XX AAW22410 standard; Protein; 140 AA.
 XX AAW22410;
 XX 08-DEC-1997 (first entry)
 XX Alpha-4 integrin mouse Mab 21.6 VH region.
 XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
 KW transplant rejection; graft versus host disease; nephritis;
 KW atopic dermatitis; psoriasis; myocardial ischaemia;
 XX acute leukocyte mediated lung injury; therapy.
 XX Mus musculus.
 XX Key Location/Qualifiers
 XX Peptide 1..19
 XX Region /label= Leader
 XX /label= FR1
 XX /note= "framework region 1"
 XX /label= CDR1
 XX /note= "complementarity determining region 1"
 XX /label= FR2
 XX /note= "framework region 2"
 XX /label= CDR2
 XX /note= "complementarity determining region 2"
 XX /label= FR3
 XX /note= "framework region 3"
 XX /label= CDR3
 XX /note= "complementarity determining region 3"
 XX /label= FR4
 XX /note= "framework region 4"
 XX WO9718838-A1.
 XX 29-MAY-1997.
 XX 21-NOV-1996; 96WO-US18807.
 XX 21-NOV-1995; 95US-0561521.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 XX Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
 XX WPI; 1997-297879/27.
 XX N-PSDB; AAT74760.
 XX Uses of humanised alpha-4 integrin antibody - for treatment of
 XX asthma, atherosclerosis, AIDS, dementia, etc.
 XX Claim 18; Page 69-70; 107pp; English.
 XX This polypeptide comprises the heavy chain variable region (VH) of
 CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
 CC complementarity determining regions (CDRs) of the 21.6 VH can be
 CC incorporated into a human 21/28'CL framework to produce a claimed
 CC humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
 CC antibody that is used in the manufacture of a medicament for
 CC treating a disease selected from asthma, atherosclerosis, AIDS,
 CC dementia, diabetes, inflammatory bowel disease, rheumatoid
 CC arthritis, transplant rejection, graft versus host disease, tumour
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
 CC ischaemia, and acute leukocyte mediated lung injury. The antibody
 CC may also be used in the affinity purification of alpha-4 integrin
 CC generating idiotypic antibodies. The humanised antibodies of the
 CC invention have a half-life in the human circulation essentially
 CC equivalent to that of naturally occurring human antibodies.
 XX Sequence 140 AA;
 XX Query Match 100.0%; Score 746; DB 18; Length 140;
 XX Best Local Similarity 100.0%; Pred. No. 1e-59;
 XX Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 18.101 Seconds
(without alignments)
327.248 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	746	100.0	140	5	PCT-US95-01219-4
3	645	86.5	123	2	US-08-561-521-9
4	645	86.5	123	5	PCT-US95-01219-9
5	633	84.9	136	3	US-08-646-265A-29
6	595	79.8	136	1	US-08-024-253-2
7	593.5	79.6	137	3	US-08-836-561-31
8	593.5	79.6	137	4	US-08-434-122-31
9	584	78.3	142	2	US-08-561-521-17
10	584	78.3	142	5	PCT-US95-01219-17
11	562	75.3	125	2	US-08-561-521-44
12	562	75.3	125	5	PCT-US95-01219-44
13	554	74.3	136	3	US-08-348-548-8
14	554	74.3	136	5	PCT-US95-15716-8
15	544	72.9	123	2	US-08-561-521-11
16	544	72.9	123	5	PCT-US95-01219-11
17	528.5	70.8	120	2	US-07-934-373C-6
18	528.5	70.8	120	3	US-08-437-642B-6
19	528.5	70.8	120	4	US-08-146-206C-6
20	528.5	70.8	120	5	PCT-US93-07832-6
21	521.5	69.9	120	4	US-08-871-488A-15
22	516	69.2	121	2	US-08-822-830B-2
23	516	69.2	121	4	US-09-157-452B-2
24	513	68.8	121	2	US-08-822-830B-13
25	513	68.8	121	4	US-09-157-452B-16
26	511	68.5	120	2	US-08-950-660-2
27	511	68.5	120	5	PCT-US93-00030-2

28	511	68.5	120	5	PCT-US93-00924-2	Sequence 2, Appl
29	505.5	67.8	138	3	US-08-603-024-2	Sequence 2, Appl
30	505.5	67.8	139	1	US-08-253-877C-8	Sequence 8, Appl
31	505.5	67.8	139	2	US-08-452-164A-8	Sequence 8, Appl
32	504	67.6	254	2	US-08-792-824-4	Sequence 4, Appl
33	504	67.6	254	2	US-08-792-824-7	Sequence 7, Appl
34	504	67.6	254	2	US-08-792-824-10	Sequence 10, Appl
35	504	67.6	254	2	US-08-792-824-13	Sequence 13, Appl
36	502	67.3	136	3	US-08-646-265A-99	Sequence 99, Appl
37	500.5	67.1	118	2	US-08-232-081B-38	Sequence 38, Appl
38	498.5	66.8	113	1	US-08-207-169A-2	Sequence 2, Appl
39	494.5	66.3	118	3	US-08-767-128-22	Sequence 22, Appl
40	491.5	65.9	642	4	US-09-423-439-26	Sequence 26, Appl
41	491.5	65.9	666	4	US-09-423-439-51	Sequence 51, Appl
42	488.5	65.5	136	4	US-09-564-329A-11	Sequence 11, Appl
43	488.5	65.5	255	3	US-09-171-945-19	Sequence 19, Appl
44	483.5	64.8	139	2	US-08-182-067-10	Sequence 10, Appl
45	483.5	64.8	139	2	US-08-465-313-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-561-521-4

Query Match 100.0%; Score 746; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.3e-68;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKCSWVFFLMAVVTGVNSEVOLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRP 60
Db 1 MKCSWVFFLMAVVTGVNSEVOLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRP 60
QY 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGY 120
Db 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGY 120
QY 121 YGNYGVYANDYWGQTSVT 140
Db 121 YGNYGVYANDYWGQTSVT 140

RESULT 2

PCT-US95-01219-4

; Sequence 4, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 25-JAN-1994
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-4

Query Match 100.0%; Score 746; DB 5; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.3e-68;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKCSWVFFLMAVVTGVNSEVOLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRP 60
Db 1 MKCSWVFFLMAVVTGVNSEVOLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRP 60
QY 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGY 120
Db 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGY 120
QY 121 YGNYGVYANDYWGQTSVT 140
Db 121 YGNYGVYANDYWGQTSVT 140

RESULT 3

US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-9

Query Match 86.5%; Score 645; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.5e-58;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 EVQLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRPQGLEWIGRIDPANGYTKY 79
Db 1 EVQLQSGAELVKPGASVKLSCTASGFKNIKDTYIHCVKQRPQGLEWIGRIDPANGYTKY 60
QY 80 DPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGYGNYGVYANDYWGQTSVT 139
Db 61 DPKFGKATITADTSSNTAYLQLSLTSEDVAVYFCAREGYGNYGVYANDYWGQTSVT 120
QY 140 V 140
Db 121 V 121

RESULT 4

PCT-US95-01219-9
; Sequence 9, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 35.3535 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-4

Perfect score: 746

Sequence: 1 MKCSVMFLNAVTVGNSE.....YGNVGYAMDYWGQGVSTV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	84.9	136	11	US-09-749-873-29
2	593.5	79.6	137	15	US-10-283-349-31
3	521.5	69.9	120	15	US-10-056-794-15
4	516	69.2	121	15	US-10-252-978-2
5	513	68.8	121	15	US-10-252-978-16
6	511	68.5	120	15	US-10-095-496-1
7	502	67.3	136	11	US-09-749-873-99
8	495.5	66.4	116	11	US-09-910-483-37
9	495.5	66.4	116	11	US-09-910-483-41
10	491.5	65.9	255	10	US-09-910-059-19
11	488.5	65.5	136	9	US-09-564-329A-11
12	488.5	65.5	136	10	US-09-855-153-11
13	488.5	65.5	136	10	US-09-854-811-11
14	488.5	65.5	136	10	US-09-934-773-11
15	488.5	65.5	136	10	US-09-963-620-11

16	488.5	65.5	136	11	US-09-855-632-11	Sequence 11, Appl
17	488.5	65.5	136	12	US-10-224-720-11	Sequence 11, Appl
18	488.5	65.5	136	12	US-10-225-779-11	Sequence 11, Appl
19	488.5	65.5	136	15	US-10-225-784-11	Sequence 11, Appl
20	483.5	64.8	139	10	US-09-809-739-5	Sequence 5, Appl
21	475.5	63.7	535	10	US-09-988-851-38	Sequence 18, Appl
22	475	63.7	117	10	US-09-158-120A-18	Sequence 38, Appl
23	473.5	63.5	153	9	US-09-861-294-4	Sequence 4, Appl
24	473.5	63.5	153	12	US-10-367-506-4	Sequence 7, Appl
25	467.5	62.7	112	14	US-10-032-482-7	Sequence 11, Appl
26	466.5	62.5	120	10	US-09-910-059-11	Sequence 11, Appl
27	463	62.1	117	11	US-09-802-083-1	Sequence 1, Appl
28	463	62.1	117	12	US-10-172-785-1	Sequence 1, Appl
29	463	62.1	117	15	US-10-165-732A-1	Sequence 1, Appl
30	461	61.8	117	9	US-09-976-787-23	Sequence 23, Appl
31	461	61.8	117	10	US-09-865-198-22	Sequence 22, Appl
32	461	61.8	117	11	US-09-798-689-7	Sequence 7, Appl
33	461	61.8	238	9	US-09-976-787-29	Sequence 29, Appl
34	461	61.8	238	10	US-09-865-198-28	Sequence 28, Appl
35	461	61.8	238	11	US-09-798-689-21	Sequence 21, Appl
36	460	61.7	117	9	US-09-976-787-7	Sequence 7, Appl
37	460	61.7	117	10	US-09-865-198-7	Sequence 7, Appl
38	460	61.7	240	9	US-09-976-787-28	Sequence 28, Appl
39	460	61.7	240	10	US-09-865-198-27	Sequence 27, Appl
40	457	61.3	138	9	US-09-753-436-78	Sequence 78, Appl
41	456	61.1	468	11	US-09-785-515-7	Sequence 7, Appl
42	455	61.0	140	9	US-09-748-960-4	Sequence 4, Appl
43	455	61.0	140	15	US-10-283-349-27	Sequence 27, Appl
44	455	61.0	269	11	US-09-749-873-109	Sequence 109, Appl
45	454.5	60.9	135	12	US-10-244-821-91	Sequence 91, Appl

ALIGNMENTS

RESULT 1
US-09-749-873-29
; Sequence 29, Application US/09749873
; Publication No. US20030023045A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,873
; FILING DATE: 29-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,265
; FILING DATE: 1996-09-09
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-749-873-29

Query Match 84.9%; Score 633; DB 11; Length 136;
Best Local Similarity 89.3%; Pred. No. 3.1e-56;
Matches 125; Conservative 2; Mismatches 7; Indels 6; Gaps 2;
QY 1 MKCSWVFFLMVAVTGVNSVQLQSGAELVKPGASVKLSCTASGFIKDTYIHCVKQRP 60
Db 1 MKCSWVFFLMVAVTGVNSVQLQSGAELVKPGASVKLSCTASGFIKDTYIHCVKQRP 60
QY 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDYAVFCAREGY 120
Db 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDYAVFCAREGY 120
QY 121 YGNVGYVAMDYWGQTSVTV 140
Db 120 YVN-----QDYWGQTSVTV 134

RESULT 2
US-10-283-349-31
Sequence 31, Application US/10283349
Publication No. US20030096977A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masamichi
FURUYA, Akiko
NAKAMURA, Kazuyasu
IIDA, Akihiro
ANAZAWA, Hideharu
HANAI, No. US20030096977A1uo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-283-349-31
Query Match 79.6%; Score 593.5; DB 15; Length 137;
Best Local Similarity 82.9%; Pred. No. 2.9e-52;
Matches 116; Conservative 6; Mismatches 13; Indels 5; Gaps 1;
QY 1 MKCSWVFFLMVAVTGVNSVQLQSGAELVKPGASVKLSCTASGFIKDTYIHCVKQRP 60
Db 1 MKCSWVFFLMVAVTGVNSVQLQSGAELVKPGASVKLSCTASGFIKDTYIHCVKQRP 60
QY 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDYAVFCAREGY 120
Db 61 EQGLEWIGRIDPANGYTKYDPKFGKATITADTSSNTAYLQLSLTSEDYAVFCAREGY 120
QY 121 YGNVGYVAMDYWGQTSVTV 140
Db 117 -GGLRLRFDFYWGQGTTLTV 135
RESULT 3
US-10-056-794-15
Sequence 15, Application US/10056794
Publication No. US20030119078A1
GENERAL INFORMATION:
APPLICANT: Graves, Scott S.
Reno, John M.
Mallett, Robert W.
Hylarides, Mark D.
Searle, Stephen M.J.
Henry, Andrew H.
Pedersen, Jan T.
Rees, Anthony R.
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE
ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN
PRETARGETING METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,794
FILING DATE: 24-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey Ph.D., Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 690022.527C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Result No.	Query			ID	Description
	Score	Match	Length		
1	603.5	80.9	178	2	S29594
2	597	80.0	136	2	S04576
3	570.5	76.5	137	2	S52445
4	567.5	76.1	123	2	PH1403
5	539	72.3	120	2	S03471
6	523	70.1	117	2	PH1586
7	521.5	69.9	122	2	S06823
8	515	69.0	115	2	S03482
9	500	67.0	116	2	S24289
10	498.5	66.8	120	2	S03484
11	494.5	66.3	268	2	A56446
12	493.5	66.2	108	2	PH1012
13	492	66.0	221	2	S49220
14	472.5	63.3	114	4	A47271
15	471	63.1	140	2	PH1482
16	467	62.6	107	2	PH1013
17	466.5	62.5	139	2	S00024
18	464.5	62.3	139	1	PMWS18
19	462.5	62.0	99	2	D37262
20	461.5	61.9	115	2	PL0246
21	461.5	61.9	139	2	A27609
22	460.5	61.7	141	2	JL0076
23	459	61.5	135	2	PH1492
24	459	61.3	140	1	HWMSG7
25	457.5	61.3	107	2	A27646
26	457	61.3	138	2	E35133
27	456	61.1	249	2	S41374
28	455.5	61.1	141	2	A39276
29	455	61.0	140	2	PH1498

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:02:30 ; Search time 10.4546 Seconds
(without alignments)
629.141 Million cell updates/sec

Title: US-09-155-739-4

Perfect score: 746

Sequence: 1 MKCSWVFFLMVTVGNSE.....YGNVGYVMDYWGQTSVTV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	464.5	62.3	139	1 HV07_MOUSE	P01751 mus musculus
2	459	61.5	140	1 HV02_MOUSE	P01746 mus musculus
3	425	57.0	120	1 HV03_MOUSE	P01747 mus musculus
4	422.5	56.6	137	1 HV11_MOUSE	P01755 mus musculus
5	416	55.8	138	1 HV48_MOUSE	P03980 mus musculus
6	411	55.1	117	1 HV09_MOUSE	P01753 mus musculus
7	396	53.1	136	1 HV15_MOUSE	P01759 mus musculus
8	393	52.7	117	1 HV06_MOUSE	P01750 mus musculus
9	393	52.7	117	1 HV49_MOUSE	P06328 mus musculus
10	389	52.1	117	1 HV10_MOUSE	P01754 mus musculus
11	388	52.0	117	1 HV04_MOUSE	P01748 mus musculus
12	381	51.1	117	1 HV52_MOUSE	P06327 mus musculus
13	379	50.8	117	1 HV13_MOUSE	P01757 mus musculus
14	379	50.8	121	1 HV01_MOUSE	P01745 mus musculus
15	378.5	50.7	147	1 HV1C_HUMAN	P01744 homo sapien
16	374	50.1	117	1 HV05_MOUSE	P01749 mus musculus
17	374	50.1	117	1 HV12_MOUSE	P01756 mus musculus
18	372	49.9	117	1 HV14_MOUSE	P01758 mus musculus
19	368.5	49.4	118	1 HV51_MOUSE	P06330 mus musculus
20	367	49.2	117	1 HV1B_HUMAN	P01743 homo sapien
21	360.5	48.3	120	1 HV50_MOUSE	P06329 mus musculus
22	359	48.1	117	1 HV1G_HUMAN	P23083 homo sapien
23	356.5	47.8	136	1 HV16_MOUSE	P01783 mus musculus
24	321.5	43.1	114	1 HV00_MOUSE	P01741 mus musculus
25	316.5	42.4	119	1 HV38_MOUSE	P01808 mus musculus
26	315	42.2	117	1 HV42_MOUSE	P01812 mus musculus
27	314	42.1	117	1 HV1A_HUMAN	P01742 homo sapien
28	312.5	41.9	119	1 HV37_MOUSE	P01807 mus musculus
29	311	41.7	142	1 HV01_RAT	P01805 rattus norv
30	310.5	41.6	119	1 HV40_MOUSE	P01810 mus musculus
31	304	40.8	118	1 HV39_MOUSE	P01809 mus musculus
32	297	39.8	117	1 HV46_MOUSE	P01822 mus musculus
33	297	39.8	144	1 HV26_MOUSE	P01795 mus musculus

34	293.5	39.3	120	1 HV1H_HUMAN	P80421 homo sapien
35	292	39.1	117	1 HV41_MOUSE	P01811 mus musculus
36	291.5	39.1	116	1 HV05_CARAU	P19181 carassius a
37	290	38.9	116	1 HV36_MOUSE	P01806 mus musculus
38	290	38.9	123	1 HV24_MOUSE	P01793 mus musculus
39	288	38.6	117	1 HV3C_HUMAN	P01764 homo sapien
40	285.5	38.3	116	1 HV3T_HUMAN	P01781 homo sapien
41	284.5	38.1	122	1 HV3G_HUMAN	P01768 homo sapien
42	284	38.1	144	1 HV43_MOUSE	P01819 mus musculus
43	284	38.1	146	1 HV2I_HUMAN	P06331 homo sapien
44	282.5	37.9	122	1 HV3A_HUMAN	P01762 homo sapien
45	282	37.8	125	1 HV1F_HUMAN	P06326 homo sapien

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M.; Paskind M.; Reth M.; Imanishi-Kari T.; Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACEYL
CC (NPB ANTIBODIES).

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).

EMBL: J00529; AAA38170.1; -.
FIR; A90809; MHMS18.
PDB; 1A6U; 27-MAY-98.
PDB; 1A6W; 15-JUL-98.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; P50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Qy	61	EGLEWIGRIDPANGYKYDKFGOKATITADSSNTAYLQLSLTSEDSTANYFCAREG	120
Db	61	GRGLEWIGRIDPNSGGTYNEKFSKATLTVDKPSSTAYMQLSSLTSEDSAVYICARYD	120
Qy	121	YGNVGYAMDYWGQGSTVTV	140
Db	121	YGS---SYDYGWGGTILTV	137

RESULT 3
HV03_MOUSE
ID HV03
AC P017
DT 21-03
DT 21-03
DT 15-03

QY	21	VQLOQSGAEVLVPGASVKLSCTASGFIKIDTIVHCVKRPEQGLEWIGRIDPANGYTKYD	80
Db	1	VQLOQSGAEVLVRAAGSSVKMSCKASGYTFSYGINVVKRPGQGLEWIGYINPGNGYTKYN	60
QY	81	PKFOCKATITADTSSNTFAYLQLSLSSLEDTAVYFCAREGYGNYGVYAMDYWGQSTVTV	14
Db	61	EKFGKTLTKDKSSPAYVQLSLSSLESDSAVYFCARSVYVG--GSYFDYWGQSTTVTV	11

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:01:50 ; Search time 46.2545 Seconds
(without alignments)
363.748 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQWTQSPSSLSASVGRVT.....YCLQYDNLWTFGGQTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA1986.DAT.*
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23: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSL1/cgcdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	106	AA1981321	Humanized anti-VLA
2	562	100.0	106	AA1981321	Humanised alpha-4
3	562	100.0	126	AA1981328	Humanised alpha-4
4	508	90.4	106	AA1981328	Mouse anti-VLA-4 a
5	508	90.4	126	AA1981328	Mouse VLA-4 antibo
6	508	90.4	126	AA1981328	Human VLA-4 reshap
7	508	90.4	126	AA1981328	Alpha-4 integrin m
8	488	86.8	359	AA1981328	Human MCP-3 and mu
9	488	86.8	361	AA1981321	Human IP-10 and mu

10	488	86.8	374	20	AA1981321	Artificial synthet
11	481	85.6	128	15	AA1981321	ME1-14 light chain
12	475.5	84.6	234	12	AA1981321	CD4-specific CDR-g
13	471.5	83.9	107	16	AA1981321	Light chain variab
14	465	82.7	108	17	AA1981321	Murine monoclonal
15	460.5	81.9	128	11	AA1981321	Variable region of
16	460	81.9	637	13	AA1981321	(FRP51)-ETA fusion
17	456	81.1	109	19	AA1981321	Anti-gp54 MAB T16
18	455	81.0	240	16	AA1981321	Anti-gp54 MAB T16
19	455	81.0	241	20	AA1981321	Amino acid sequenc
20	455	81.0	245	19	AA1981321	Anti-gp54 MAB T16
21	453.5	80.7	107	18	AA1981321	Humanised VLA-4 an
22	453.5	80.7	107	18	AA1981321	Humanised alpha-4
23	453	80.6	109	12	AA1981321	Murine OKT4A light
24	452	80.4	241	13	AA1981321	FWP51 fusion prote
25	451.5	80.3	108	16	AA1981321	Human REI monoclon
26	451.5	80.3	129	15	AA1981321	Human/murine II-1
27	451	80.2	355	18	AA1981321	R. pipiens recombi
28	449.5	80.0	107	19	AA1981321	Variable Light dom
29	449.5	80.0	107	19	AA1981321	Humanised murine a
30	449.5	80.0	107	23	AA1981321	Humanised anti-VEG
31	446.5	79.4	108	18	AA1981321	CDR-grafted light
32	446.5	79.4	110	19	AA1981321	Anti-VEGF humanise
33	446.5	79.4	110	23	AA1981321	Humanised anti-VEG
34	446.5	79.4	234	18	AA1981321	TF8-5G9 CDR-grafte
35	446.5	79.4	237	19	AA1981321	Protein encoded by
36	446.5	79.4	650	23	AA1981321	Phage-display anti
37	445.5	79.3	107	19	AA1981321	Variable Light dom
38	445.5	79.3	107	19	AA1981321	Humanised murine a
39	445.5	79.3	107	23	AA1981321	Humanised anti-VEG
40	444.5	79.1	107	20	AA1981321	Humanised anti-alp
41	444.5	79.1	107	22	AA1981321	Human VI consensus
42	444.5	79.1	107	22	AA1981321	Consensus human 11
43	444.5	79.1	107	22	AA1981321	Human variable lig
44	444.5	79.1	108	19	AA1981321	Human consensus fr
45	444.5	79.1	108	21	AA1981321	Human consensus se

ALIGNMENTS

RESULT 1
AA1981321
ID AA1981321 standard; Protein; 106 AA.
AC AA1981321;
XX
XX 02-APR-1996 (first entry)
DT
DE Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
XX Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
XX antibody engineering.
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
PW WO9519790-A1.
XX
XX 27-JUL-1995.
XX
XX 25-JAN-1995; 95WO-US01219.
XX
XX 25-JAN-1994; 94US-0186269.
XX
XX (ATHE-) ATHENA NEUROSCIENCES INC.
PA Bendig MM, Jones TS, Leger OJ, Saldanha J;
PI WPI; 1995-269276/35.
DR
XX New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating

PT inflammatory disease.

PS Claim 9; Page 67; 105pp; English.

XX The sequence encodes the humanized mouse antibody 21.6 light chain
 CC variable region, La, directed against leukocyte adhesion molecule
 CC VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
 CC AAQ99892) regions are linked to human constant regions in the
 CC construction of a humanized antibody against VLA-4. The 5' and 3'
 CC ends of the mouse cDNAs are modified using PCR primers (See
 CC AAQ99895-98) and then subcloned into mammalian cell expression vectors
 CC containing human kappa or gamma-1 constant regions. In the humanized
 CC light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
 CC VR framework are replaced by the amino acid present in the equivalent
 CC position of the mouse 21.6 lg L chain. Plasmids encoding the chimeric
 CC antibodies are transfected into COS cells. The humanized antibodies
 CC can be used for inhibiting adhesion of a leukocyte to an endothelial
 CC cell and for treating inflammatory diseases such as multiple
 CC sclerosis. They can also be used in the treatment of stroke,
 CC cerebral traumas, meningitis or encephalitis. The antibodies can
 CC also be used for detecting VLA-4, for affinity purification or for
 CC generating anti-idiotypic antibodies.

XX Sequence 106 AA;

SQ Query Match 100.0%; Score 562; DB 16; Length 106;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-36;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYAWYQQTGKAPRLLIHYTSLALQGPIS 60

DB 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYAWYQQTGKAPRLLIHYTSLALQGPIS 60

QY 61 RFGSGSGRDYTFITSLQPEDIATYYCLOYDNLWTFGQGTKEIK 106

DB 61 RFGSGSGRDYTFITSLQPEDIATYYCLOYDNLWTFGQGTKEIK 106

RESULT 2

ID AAW22412
 AC AAW22412 standard; Protein; 106 AA.

XX AAW22412;

DT 08-DEC-1997 (first entry)

XX Humanised alpha-4 integrin antibody 21.6 VL La.

XX Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
 KW transplant rejection; graft versus host disease; nephritis;
 KW atopic dermatitis; psoriasis; myocardial ischaemia;
 KW acute leukocyte mediated lung injury; therapy.

XX Chimeric Mus musculus;

OS Chimeric Homo sapiens;

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Region 1..23

FT /label= FR1

FT /note= "REI framework region 1"

FT Region 24..34

FT /label= CDR1

FT /note= "21.6 complementarity determining region 1"

FT Region 35..49

FT /label= FR2

FT /note= "REI framework region 2"

FT Misc-difference 45

FT /note= "REI Lys-45 is substd. by Lys of mouse

FT 21.6 VL, important in supporting the

FT CDR2 loop"

XX Sequence 106 AA;

FT Misc-difference 49
 FT /note= "REI Tyr-49 is substd. by His of mouse
 FT 21.6 VL, located at the binding site"
 FT Region 50..56
 FT /label= CDR2
 FT /note= "21.6 complementarity determining region 2"
 FT Region 57..88
 FT /label= FR3
 FT /note= "REI framework region 3"
 FT Misc-difference 58
 FT /note= "REI Val-58 is substd. by Ile of mouse
 FT 21.6 VL, important in supporting the CDR2
 FT loop"
 FT Misc-difference 69
 FT /note= "REI Thr-69 is substd. by Arg of mouse
 FT 21.6 VL, involved in antibody-antigen
 FT binding"
 FT Region 89..96
 FT /label= CDR3
 FT /note= "21.6 complementarity determining region 3"
 FT Region 97..106
 FT /label= FR4
 FT /note= "REI framework region 4"
 FT Misc-difference 103
 FT /note= "REI Leu-103 substd. by Val, more typical
 FT of human kappa light chain J region"
 FT Misc-difference 104
 FT /note= "REI Gln-104 substd. by Glu, more typical
 FT of human kappa light chain J region"
 FT Misc-difference 106
 FT /note= "REI Thr-106 substd. by Lys, more typical
 FT of human kappa light chain J region"
 XX WO9718838-A1.
 XX 29-MAY-1997.
 XX 21-NOV-1996; 96WO-US18807.
 XX 21-NOV-1995; 95US-0561521.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 XX Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
 XX WPI: 1997-297879/27.
 XX Uses of humanised alpha-4 integrin antibody - for treatment of
 XX asthma, atherosclerosis, AIDS, dementia, etc.
 XX Claim 25; Fig 6; 107pp; English.
 XX This polypeptide, designated La, comprises the light chain variable
 XX region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
 XX composed of complementarity determining regions (CDRs) from the VL
 XX region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
 XX 21.6 and a modified human REI framework. It can be expressed in
 XX mammalian host cells following PCR amplification and mutagenesis
 XX of appropriate fragments of mouse and human DNA sequences. The
 XX humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
 XX to produce a claimed humanised 21.6 antibody that is useful in the
 XX manufacture of a medicament for treating asthma, atherosclerosis,
 XX AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
 XX arthritis, transplant rejection, graft versus host disease, tumour
 XX metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
 XX ischaemia, and acute leukocyte mediated lung injury. The antibody
 XX may also be used in the affinity purification of alpha-4 integrin
 XX for use as a vaccine or an immunogen. It is also useful for
 XX generating idiotypic antibodies. The humanised antibody has a
 XX half-life in the human circulation essentially equivalent to that
 XX of naturally occurring human antibodies.

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 13.7051 Seconds

(without alignments)
327.248 Million cell updates/sec

Title: US-09-155-739-7

Perfect score: 562

Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLMTFGGTRKVEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	508	90.4	106	5	PCT-US95-01219-5
5	508	90.4	126	2	US-08-561-521-2
6	508	90.4	126	2	US-08-561-521-15
7	508	90.4	126	5	PCT-US95-01219-2
8	508	90.4	126	5	PCT-US95-01219-15
9	488	86.8	359	4	US-09-646-028-16
10	488	86.8	361	4	US-09-646-028-13
11	488	86.8	374	4	US-09-646-028-15
12	481	85.6	128	1	US-08-339-582-4
13	471.5	83.9	107	2	US-08-888-366-22
14	460	81.9	637	1	US-08-235-838-16
15	460	81.9	637	2	US-08-465-473B-16
16	455	81.0	241	1	US-08-235-838-11
17	455	81.0	241	2	US-08-465-473B-11
18	454.5	80.9	108	2	US-08-602-725-29
19	453.5	80.7	107	2	US-08-561-521-8
20	453.5	80.7	107	5	PCT-US95-01219-8
21	451	80.2	355	3	US-08-875-811-57
22	448.5	79.8	107	2	US-07-934-373C-17
23	448.5	79.8	107	3	US-08-437-642B-17
24	448.5	79.8	107	4	US-08-146-206C-17
25	448.5	79.8	107	5	PCT-US93-07832-17
26	444.5	79.1	107	2	US-07-934-373C-18
27	444.5	79.1	107	3	US-08-437-642B-18

28 444.5 79.1 107 4 US-08-146-206C-18 Sequence 18, Appl
29 444.5 79.1 107 5 PCT-US93-07832-18 Sequence 18, Appl
30 444.5 79.1 108 3 US-08-974-899-3 Sequence 3, Appl
31 444.5 79.1 111 1 US-08-137-117D-67 Sequence 67, Appl
32 444.5 79.1 111 2 US-08-436-717-67 Sequence 67, Appl
33 444.5 79.1 126 1 US-08-137-117D-71 Sequence 71, Appl
34 444.5 79.1 126 2 US-08-436-717-71 Sequence 71, Appl
35 443.5 78.9 107 2 US-08-561-521-6 Sequence 6, Appl
36 443.5 78.9 107 2 US-08-652-558-34 Sequence 34, Appl
37 443.5 78.9 107 4 US-09-025-203-15 Sequence 15, Appl
38 443.5 78.9 107 5 PCT-US95-01219-6 Sequence 6, Appl
39 443.5 78.9 108 2 US-08-070-116A-7 Sequence 7, Appl
40 443.5 78.9 108 2 US-08-116-247-9 Sequence 9, Appl
41 443.5 78.9 108 4 US-08-557-050-7 Sequence 7, Appl
42 441.5 78.6 107 2 US-08-318-157B-6 Sequence 6, Appl
43 440.5 78.4 107 2 US-08-652-558-2 Sequence 2, Appl
44 440.5 78.4 109 2 US-07-934-373C-3 Sequence 3, Appl
45 440.5 78.4 109 3 US-08-437-642B-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-7

Query Match 100.0%; Score 562; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.6e-45;
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RESULT 2
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

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QY 61 RFGSGSRDYFTFISSLOPEDIATYYCLOYDNLWTFGGTKVEIK 106
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nb 61 RFGSGSRDYFTFISSLOPEDIATYYCLOYDNLWTFGGTKVEIK 106

RESULT 3
US-08-561-521-5
; Sequence 5,-Application US/08561521
; Patent No. 5840299

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1  GENERAL INFORMATION:
2  APPLICANT: Bendig, Mary M.
3  APPLICANT: Leger, Olivier J.
4  APPLICANT: Saldanha, Jose
5  APPLICANT: Jones, S. Tarran
6  TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
7  TITLE OF INVENTION: Adhesion Molecule VLA-4
8  NUMBER OF SEQUENCES: 45
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Townsend and Townsend Kourile and Crew
11 STREET: One Market Plaza, Steuart Tower, Suite 2000
12 CITY: San Francisco
13 STATE: California
14 COUNTRY: USA
15 ZIP: 94105
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/561,521
23 FILING DATE:
24 CLASSIFICATION: 424
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/08/186,269A
27 FILING DATE: 25-JAN-1994
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Smith, William L.
30 REGISTRATION NUMBER: 30,223
31 REFERENCE/DOCKET NUMBER: 15270-14
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 415-543-9600
34 TELEFAX: 415-543-5043
35 INFORMATION FOR SEQ ID NO: 5:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 106 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: protein
42 US-08-561-521-5

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RESULT 4
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 26.7677 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQYDNLWTFGQTKVEIK 106

Scoring table:
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Total number of hits satisfying chosen parameters: 587654

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	466.5	83.0	108	9	US-09-229-200A-16
7	449.5	80.0	107	9	US-09-056-160B-15
8	446.5	79.4	110	9	US-09-056-160B-103
9	446.5	79.4	237	9	US-09-056-160B-100
10	446.5	79.4	491	14	US-10-011-125-2
11	445.5	79.3	107	9	US-09-056-160B-13
12	444.5	79.1	107	12	US-10-223-880-15
13	444.5	79.1	107	15	US-10-268-501-5
14	444.5	79.1	108	9	US-09-056-160B-12
15	444.5	79.1	109	9	US-09-811-123-6

16	444.5	79.1	110	12	US-10-044-896-4	Sequence 4, Appli
17	443.5	78.9	107	10	US-09-959-025-15	Sequence 15, Appl
18	443.5	78.9	107	10	US-09-939-040-15	Sequence 15, Appl
19	443.5	78.9	107	11	US-09-998-817-15	Sequence 15, Appl
20	443.5	78.9	107	11	US-09-999-021-15	Sequence 15, Appl
21	443.5	78.9	107	15	US-10-040-997-15	Sequence 15, Appl
22	443.5	78.9	108	9	US-09-229-200A-14	Sequence 14, Appl
23	443.5	78.9	108	15	US-10-267-286A-7	Sequence 7, Appli
24	443.5	78.9	110	9	US-09-056-160B-105	Sequence 105, App
25	443	78.8	109	9	US-09-229-200A-7	Sequence 7, Appli
26	442.5	78.7	108	9	US-09-056-160B-8	Sequence 8, Appli
27	442.5	78.7	108	14	US-10-153-159-2	Sequence 2, Appli
28	442.5	78.7	108	14	US-10-153-159-16	Sequence 16, Appl
29	442.5	78.7	108	15	US-10-153-176-2	Sequence 2, Appli
30	442.5	78.7	108	15	US-10-153-176-16	Sequence 16, Appl
31	442.5	78.7	131	15	US-10-207-655-256	Sequence 256, App
32	442.5	78.7	266	15	US-10-207-655-260	Sequence 260, App
33	442.5	78.7	550	15	US-10-207-655-270	Sequence 270, App
34	441.5	78.6	107	9	US-09-253-794-6	Sequence 6, Appli
35	439.5	78.2	108	14	US-10-153-159-4	Sequence 4, Appli
36	439.5	78.2	108	15	US-10-153-176-4	Sequence 4, Appli
37	439.5	78.2	110	9	US-09-056-160B-107	Sequence 107, App
38	439.5	78.2	110	9	US-09-056-160B-117	Sequence 117, App
39	439.5	78.2	237	15	US-10-020-786-10	Sequence 10, Appl
40	438.5	78.0	108	9	US-09-905-243-73	Sequence 73, Appl
41	438.5	78.0	109	11	US-09-802-083-4	Sequence 4, Appli
42	438.5	78.0	109	12	US-10-172-785-4	Sequence 4, Appli
43	438.5	78.0	109	15	US-10-165-732A-4	Sequence 4, Appli
44	438.5	78.0	127	10	US-09-809-739-10	Sequence 10, Appl
45	438.5	78.0	214	9	US-09-940-166A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-335-394-16
; Sequence 16, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; PRIOR FILING DATE: 2002-12-31
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct
US-10-335-394-16

Query Match	86.8%;	Score 488;	DB 12;	Length 359;
Best Local Similarity	84.9%;	Pred. No. 8.7e-37;		
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Db	233	DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWQHKGKPRLLIIHYTSLQPGIPS 292		
QY	61	REFSGSGRDYFTFTISSLPEDIATYYCIQYDNLWTFGQTKVEIK 106		
Db	293	REFSGSGRDYFISINLEPEDIATYYCIQYDNLWTFGQTKLEIK 338		

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RESULT 2
US-10-335-394-13
; Sequence 13, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-13

Query Match      86.8%; Score 488; DB 12; Length 361;
Best Local Similarity 84.9%; Pred. No. 8.7e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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Db      235 DIQMTQSPSSLSASVGRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 294

Qy      61 RFSGSGGRDYFTFTISSLPEDIATYYCYLDNLTFTGGQTKVEIK 106
Db      295 RFSGSGGRDYFTFTISSLPEDIATYYCYLDNLTFTGGQTKLEIK 340

RESULT 3
US-10-335-394-15
; Sequence 15, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-15

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Best Local Similarity 84.9%; Pred. No. 9.1e-37;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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RESULT 4
US-09-229-200A-11
; Sequence 11, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229,200A
; FILING DATE: 13-Jan-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Wallen, III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: ORT-948
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 784-3239
; TELEFAX: (908) 524-2808
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-229-200A-11

Query Match      85.3%; Score 479.5; DB 9; Length 108;
Best Local Similarity 85.8%; Pred. No. 1.5e-36;
Matches 91; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

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Db      1 DIQMTQSPSSLSASVGRVTITCKTSQDINKYMAWYQOTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGGRDYFTFTISSLPEDIATYYCYLDNLTFTGGQTKVEI 105
Db      61 RFSGSGGCTDFTFTISSLPEDIATYYCYLDNLTFTGGQTKLQI 106

RESULT 5
US-09-229-200A-15
; Sequence 15, Application US/09229200A
; Patent No. US20020099179A1
; GENERAL INFORMATION:
; APPLICANT: Jolliffe et al.
; TITLE OF INVENTION: CD4 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One Johnson & Johnson Plaza
; CITY: New Brunswick
; STATE: NJ
; COUNTRY: USA
; ZIP: 08933-7003
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:09:40 ; Search time 14.9899 seconds
(without alignments)
680.050 Million cell updates/sec

Title: US-09-155-739-7

Perfect score: 562

Sequence: 1 DIQMTQSPSSLSASVGRVT.....YCLQYDNLMTFGQGTKEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	488	86.8	104	2	S26330 Ig kappa chain V r
2	479	85.2	104	2	S26329 Ig kappa chain V r
3	478	85.1	106	2	C35936 Ig kappa chain V r
4	463.5	82.5	125	2	S09365 Ig kappa chain - m
5	452	80.4	97	2	PH1064 Ig light chain V r
6	446.5	79.4	107	2	PI0270 Ig kappa chain V r
7	443.5	78.9	108	1	KIHURE Ig kappa chain V-I
8	443.5	78.9	129	2	S22789 Ig kappa chain V r
9	443	78.8	103	2	S26332 Ig light chain V r
10	440.5	78.4	107	2	PL0272 Ig kappa chain V r
11	440	78.3	94	2	E33730 Ig kappa chain V r
12	439.5	78.2	107	2	PI0269 Ig kappa chain V r
13	439.5	78.2	107	2	PI0271 Ig kappa chain V-I
14	439.5	78.2	108	1	KIHURU Ig kappa chain V-I
15	435.5	77.5	110	2	I39154 Ig kappa chain (BR
16	429.5	76.4	110	2	S40331 Ig kappa chain V-J
17	429.5	76.4	127	2	S40367 Ig kappa chain V-J
18	426	75.8	107	2	S36275 Ig lambda chain V
19	424.5	75.5	125	2	S40333 Ig kappa chain V-J
20	421.5	75.0	108	1	KIHULY Ig kappa chain V-I
21	419.5	74.6	108	1	KIHUAG Ig kappa chain V-I
22	419.5	74.6	108	1	KIHURY Ig kappa chain V-I
23	418.5	74.5	123	2	S40331 Ig kappa chain - h
24	415.5	73.9	109	2	S31998 Ig kappa chain - h
25	414.5	73.8	131	2	S40352 Ig kappa chain V-J
26	414	73.7	124	2	S40336 Ig kappa chain V-J
27	413.5	73.6	108	1	KIHUSW Ig kappa chain V-I
28	412.5	73.4	108	2	B49047 Ig kappa chain V r
29	412	73.3	106	2	PC2397 anti-tetanus toxin

ALIGNMENTS

RESULT 1

S26330

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26330

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26330

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

A:Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 86.8%; Score 488; DB 2; Length 104;

Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCKTSODINKYMQQTPGKAPRLLIHYTSALQPGIPS 60

Db 1 DIQMTQSPSSLSASLGGRVTITCKASQDINKYIAWYQHKPGKGRPLLIIHYTSALQPGIPS 60

OY 61 RFSGSGSGRDYFTFTISSLPEDIATYYCLQYDNLMTFGQGTKE 104

Db 61 RFSGSGSGRDYFTFTISSLPEDIATYYCLQYDNLMTFGQGTKE 104

RESULT 2

S26329

Ig kappa chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C:Accession: S26329

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protei

A:Reference number: S26309; MUID:91341421; PMID:1908510

A:Accession: S26329

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-104 <STA>

A:Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.2%; Score 479; DB 2; Length 104;

Best Local Similarity 84.6%; Pred. No. 9.8e-35;
Matches 88; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSLQPGIPS 60
|||||
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSLQPGIPS 60
QY 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKVE 104
|||||
Db 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKLE 104

RESULT 3

C33936

Ig kappa chain V region (VMI13) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C;Accession: C33936

R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.

Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989

A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene

A;Reference number: A33936; MUID:89282831; PMID:2471975

A;Accession: C33936

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-106 <MEE>

A;Cross-references: GB:J04577; NID:g623187; PID:AAA60443.1; PID:g623189

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 478; DB 2; Length 106;

Best Local Similarity 83.0%; Pred. No. 1.2e-34;

Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSLQPGIPS 60
|||||
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSLQPGIPS 60
QY 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKVEIK 106
|||||
Db 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKLEIK 106

RESULT 4

S09365

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S09365

R;Feddersen, R.; van Ness, B.

Nucleic Acids Res. 17, 9797-9809, 1989

A;Title: Direct evidence for intrastand DNA inversion of kappa immunoglobulin gene segm

A;Reference number: S09365; MUID:90098844; PMID:2513557

A;Accession: S09365

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-125 <FED>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 463.5; DB 2; Length 125;

Best Local Similarity 83.2%; Pred. No. 2.6e-33;

Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSLQPGIPS 60
|||||
Db 18 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSLQPGIPS 77
|||||

QY 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKVEIK 106
|||||

Db 78 RFGSGSGSDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKLEIK 124

RESULT 5

PHI064

Ig light chain V region (clone 202.54) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Accession: PHI064

R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A;Reference number: PH0971; MUID:92381444; PMID:1512540

A;Accession: PHI064

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-97 <TIL>

C;Experimental source: B cell, strain [NZB x NZW]F1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 452; DB 2; Length 97;

Best Local Similarity 85.6%; Pred. No. 2e-32;

Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSLQPGIPS 60
|||||
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSLQPGIPS 60
QY 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTF 97
|||||

Db 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTF 97

RESULT 6

PL0270

Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C;Accession: PL0270

R;Slomchuk, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein

J. Exp. Med. 171, 285-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A;Reference number: PL0231; MUID:9011618; PMID:2104919

A;Accession: PL0270

A;Molecule type: mRNA

A;Residues: 1-107 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-90/Domain: immunoglobulin homology <IMM>

F;24-34/Region: complementarity-determining 1

F;33-49/Region: complementarity-determining 2

F;50-56/Region: complementarity-determining 2

F;57-88/Region: complementarity-determining 3

F;89-97/Region: complementarity-determining 3

F;98-107/Region: complementarity-determining 4

Query Match 79.4%; Score 446.5; DB 2; Length 107;

Best Local Similarity 79.4%; Pred. No. 6.5e-32;

Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITCKTSQDINKYMAWYQQTGKAPRLLIHYTSLQPGIPS 60
|||||
Db 1 DIQMTQSPSSLSASLGKVTITCKASQDINKYIAWYQHKPGKPRLLIHYTSLQPGIPS 60
QY 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKVEIK 106
|||||

Db 61 RFGSGSGRDYNTFTISSLOPEDATYCYCLQYDNLWTFGGQTKLEIK 107

RESULT 7

K1HURE

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:02:30 ; Search time 7.92323 Seconds
(without alignments)
629.141 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQWTQSPSLASVGRVT.....YCLQYDNLWTFGQTKVEIK 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	443.5	78.9	108	1 KV10_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1 KV1B_HUMAN	P01594 homo sapien
3	431.5	75.0	108	1 KV1M_HUMAN	P01605 homo sapien
4	419.5	74.6	108	1 KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1 KV1P_HUMAN	P01608 homo sapien
6	419.5	74.6	108	1 KV1Y_HUMAN	P80362 homo sapien
7	413.5	73.6	108	1 KV1Q_HUMAN	P01609 homo sapien
8	409.5	72.9	129	1 KV1W_HUMAN	P04431 homo sapien
9	409	72.8	107	1 KV1D_HUMAN	P01596 homo sapien
10	408.5	72.7	108	1 KV1R_HUMAN	P01610 homo sapien
11	402.5	71.6	108	1 KV1H_HUMAN	P01600 homo sapien
12	397.5	70.7	108	1 KV1F_HUMAN	P01598 homo sapien
13	396.5	70.6	108	1 KV1V_HUMAN	P04430 homo sapien
14	390.5	69.5	108	1 KV1G_HUMAN	P01603 homo sapien
15	388.5	69.1	108	1 KV1E_HUMAN	P01597 homo sapien
16	386.5	68.8	108	1 KV1L_HUMAN	P01604 homo sapien
17	385.5	68.6	108	1 KV1N_HUMAN	P01606 homo sapien
18	384.5	68.4	108	1 KV1C_HUMAN	P01595 homo sapien
19	383.5	68.2	108	1 KV1G_HUMAN	P01599 homo sapien
20	383.5	68.2	129	1 KV1X_HUMAN	P04432 homo sapien
21	381.5	67.9	108	1 KV1S_HUMAN	P01611 homo sapien
22	376.5	67.0	134	1 KV4C_HUMAN	P06314 homo sapien
23	371.5	66.1	108	1 KV5U_MOUSE	P01643 mus musculus
24	368	65.5	117	1 KV1J_HUMAN	P01602 homo sapien
25	366.5	65.2	128	1 KV5E_MOUSE	P01637 mus musculus
26	365	64.9	133	1 KV4B_HUMAN	P06313 homo sapien
27	364.5	64.9	108	1 KV5Q_MOUSE	P01648 mus musculus
28	363.5	64.7	108	1 KV5W_MOUSE	P01647 mus musculus
29	362	64.4	109	1 KV1T_HUMAN	P01601 homo sapien
30	362	64.4	117	1 KV1I_HUMAN	P01602 homo sapien
31	361.5	64.3	108	1 KV5K_MOUSE	P01644 mus musculus
32	359.5	64.0	108	1 KV5M_MOUSE	P01646 mus musculus
33	358.5	63.8	108	1 KV5L_MOUSE	P01645 mus musculus

ALIGNMENTS

RESULT 1

ID	KV10_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01607;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain V-I region Rei.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=76023758; PubMed=809329;			
RA	Palm W., Hilschmann N.;			
RT	"The primary structure of a crystalline monoclonal immunoglobulin			
RT	kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation			
RT	and characterization of the tryptic peptides; the complete amino acid			
RT	sequence of the protein; a contribution to the elucidation of the			
RT	three-dimensional structure of antibodies, in particular their			
RT	combining site.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).			
RN	[2]			
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).			
RX	MEDLINE=76039968; PubMed=1182131;			
RA	Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;			
RT	"The molecular structure of a dimer composed of the variable portions			
RT	of the Bence-Jones protein Rei refined at 2.0-A resolution.";			
RL	Biochemistry 14:4943-4952(1975).			
CC	-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)			
CC	MARKER.			
CC	-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
DR	PIR; A91663; KIHUPE			
DR	PDB; IREI; 17-FEB-84.			
DR	PDB; IAR2; 12-NOV-97.			
DR	PDB; 1BWV; 29-DEC-99.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding activity; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; Igv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 86			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	STRAND 4 7			

34	356.5	63.4	112	1	KV1U_HUMAN	P01613 homo sapien
35	348.5	62.0	114	1	KV1A_HUMAN	P01625 homo sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207 homo sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653 mus musculus
39	345	61.4	115	1	KV5F_MOUSE	P01638 mus musculus
40	341.5	60.8	108	1	KV5Q_MOUSE	P01650 mus musculus
41	341	60.7	109	1	KV3E_HUMAN	P01623 homo sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652 mus musculus
43	339.5	60.4	108	1	KV5U_MOUSE	P04946 mus musculus
44	339	60.3	109	1	KV3D_HUMAN	P01622 homo sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624 homo sapien

```

FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 44 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT TURN 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 97 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 78.9%; Score 443.5; DB 1; Length 108;
Best Local Similarity 81.1%; Pred. No. 4.9e-40;
Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYMAWYQOTPGKAPRLIHYSALQPGIPS 60
DQ 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYMAWYQOTPGKAPRLIHYSALQPGIPS 60
QY 61 RFGSGSGRDYTFYTISSLPQEDIAFYCYCQYDNL-WTFGQGTKEIK 105
DQ 61 RFGSGSGRDYTFYTISSLPQEDIAFYCYCQYDNL-WTFGQGTKEIK 106

RESULT 2
KVLM_HUMAN
ID KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91653; KIHU.
DR PDB; 1JUV5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

```

```

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 78.2%; Score 439.5; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 1.3e-39;
Matches 85; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYMAWYQOTPGKAPRLIHYSALQPGIPS 60
DQ 1 DIQMTQSPSSLSASVGRVITCTKTSQDINKYMAWYQOTPGKAPRLIHYSALQPGIPS 60
QY 61 RFGSGSGRDYTFYTISSLPQEDIAFYCYCQYDNL-WTFGQGTKEIK 106
DQ 61 RFGSGSGRDYTFYTISSLPQEDIAFYCYCQYDNL-WTFGQGTKEIK 107

RESULT 3
KVLM_HUMAN
ID KVLM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHULY.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97

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